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GenCore version 5.1.6

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OM protein - protein search, using sw model

Pun on November 5, 2004, 18:34:11; Search time 55,4461 Seconds
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November 5, 2001, 10.1111, Common (without alignments) 3839.562 Million cell updates/sec	US-10-797-893-2 1878 1 MAAGGSTQQRRREMAAASAAFYLDTVSALNFAARSKEVIN 370
	US-10-797-893-2 1878 1 MAAGGSTQQRRRE
Kull On:	Title: US-10 Perfect score: 1878 Sequence: 1 MAA

ILLE: Perfect score: 1878 Sequence: 1 MAAGGSTQQRRREMAAASAAFYLDTVSALNFAARSKEVIN 37	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	rched: 1825181 segs, 575374646 residues	motel mimber of hite gariefying chosen parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q14807 homo sapien	Aap35923 homo sapi	Q991c7 mus musculu	Q6p3r1 xenopus tro	Aah63896 xenopus t	Q9i869 xenopus lae	Aah70549 xenopus l		xenobna	xenobna	OggpgO xenopus lae	O60845 homo sapien	035232 mus musculu	Q61512 oryza sativ	ഴ					anopheles		-		drosc	omou.	pomod.	_	plas	mus	e mus	Q8b111 mus musculu
QI	KF22 HUMAN	AAP35923	Q99LC7	Q6P3R1	AAH63896	691860	AAH70549	Q918K0	Q7ZYL5	Q919A8	Q6GPG0	060845	035232	Q6L512	AAT39162	Q8L7B8	Q9LZ88	600880	Q7RX60	Q7QDS6	Q862B6	Q961H5	QBN1X8	KL68_DROME	Q86VSS	Q8N177	Q9H0F3	Q7RM16	Q8BY99	Q8BZ45	Q8BLL1
DB	-		7											•						7		8	•	•	7	•	7	7	~	~	7
% Query Match Length	665	665	99	639	639	651	651	651	663	650	631	198	148	584	584	628			912						868	868	868	1296	562	571	880
	100.0	100.0	85.4	9.59	9.59	64.0	64.0	64.0	63.8	63.5	63.4	9.05	37.5	33.2	33.2	31.7	31.7	31.1	30.8	30.3	30.0	29.8	29.8	29.6	29.4	29.4	29.4	29.4	29.4	29.4	29.4
Score	1878	1878	1604.5	1232	1232	1202.5	1202.5	1201.5	1197.5	1192.5	1191.5	951	704	623.5	623.5	594.5	594.5	584.5	578	568.5	563	559.5	559	555.5	552.5	552.5	552.5	552	551.5	551.5	551.5
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32	16. c	36	38	39	40	41	42	43	44	4.5

ALIGNMENTS

30L		RP SEQUENCE FROM N.A. RC TISSUE-Lymphocytoblastoma; RX MEDLINE-9900323; PubMed-9790757; RA Song J., Murakami H., Yang Z.Q., Koga C., Adati N., Murata T., RA Galtinger C., Saito-Ohara F., Ikeuchi T., Matsumura M., Itakura K., RA Kanazawa I., Sun K., Yokoyama K.k.; RT "Human genes for KNSL4 and MAZ are located close to one another on RT chromosome 16pl1.2."; RI chromosome 15pl1.2."; RN (3)		
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Kinesin-like 4.
Homo sapiens (Human)
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                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the butpopan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.cib.ch).
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                                            PubMed-11146551; DOI=10.1038/sj.coc.1204002; Germani A., Bruzzoni-Giovanelli H., Fellous A., Gisselbrecht S., Varin-Blank N., Calvo F.; Sipha-Lubulin and degrades the kinesin Kid by the proteasome pathway during mitosis."; Oncogene 19:5997-6006(2000).
-: FUNCTION: Kinesin family that is involved in spindle formation and the movements of chromosomes during mitosis and meiosis. Binds to microtubules and to DNA.
-: SUBCELLULAR LOCATION: Nuclear.
-: FTM: Ubiquitinated; mediated by SIAH1 and leading to its subsequent proteasomal degradation (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                       R MIM; 603213; -
R GO; GO:0000776; C:kinetochore; TAS.
R GO; GO:0005674; C:nucleus; TAS.
R GO; GO:0005677; F:DNA binding; TAS.
R GO; GO:0007067; F:DNA binding; TAS.
R GO; GO:0007067; P:microtubule motor activity; TAS.
R GO; GO:0007067; P:microtubule motor activity; TAS.
R GO; GO:0007067; P:microtubule motor.
R InterPro; IPR001752; kinesin motor.
InterPro; IPR001752; kinesin motor.
R InterPro; IPR001994; KuvA_2 Tike.
R FAMRT; SM00219; Kinesin; 1.
R RNART; SM00219; KISC; 1.
R SMART; SM00219; KISC; 1.
R RNOSITE; PS50067; KINESIN MOTOR DOMAIN1; 1.
R RNOSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
R PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
R PROSITE; Coiled coil; DNA-binding; Microtubule; Motor protein;
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V -> A (in Ref. 2).
V >> SASSOCISPLOKISSMDPAMLERLISLDRLIASQGSQ
-> SSSICLEPETQPPTEAKAAWTRPCGAPPQLGPSACLPGE
P (in Ref. 2).
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Coiled coil (Potential).
ATP (Potential).
Missing (in Ref. 2).
S -> KV (in Ref. 2).
HTMLGSPEQPGVIPRALMDLLQLTREEGABGRPWA
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mouse cDNA sequences.";
.. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 1.2e-135;
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                                     INTERACTION WITH SIAH1, AND DEGRADATION
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AB017334 BAA33063.1; JOINED.
AB017334; BAA33063.1; JOINED.
BC004352; AAH04523.1; -.
BC028155; AAH28155.1; -.
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Moreira D., Kelley T., Labaer J., Lin Y.,
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Catarrhini, Hominidae, Homo.
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SEQUENCE 665 AA; /73261 MW; C6C0AC96741DD387 CRC64;
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Mammalia; Eutheria; Primates;
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Kalnine N., Chen X., Rolfs A
Koundinya M., Raphael J., Mo
Phelan M., Farmer A.;
"Cloning of human full|lengt:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
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Matches 370; Conservative
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Submitted (MAY-2003)
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GenCore version 5.1.6
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	November 5, 2004, 18:34:11; Search time 76.7254 Seconds (without alignments)	3839.562 Million cell updates/sec
	; Search time 76.729 (without alignments)	3839.562 Mill
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OM protein - protein search, using sw model	Run on:	

Title: US-10-797-893-4
Perfect score: 2589
Sequence: 1 MPAAGGSTQQRRREWAAASA......LEAKWLAQKAEEKENHCPTM 512

Sequence: 1 MPAAGGSTQQRRREMAAASA.. Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O14807 homo sapien	Aap35923 homo gapi	0991c7 mus musculu	Q6p3r1 xenopus tro	Aah63896 xenopus t	Q9i869 xenopus lae	Aah70549 xenopus l	Q9i8k0 xenopus lae						Q61512 oryza sativ	Aat39162 oryza sat	Q961h5 drosophila		Q91z88 arabidopsis		Q86zb6 botrytis ci					Q9vrk9 drosophila			Q91784 xenopus lae	Q6irm2 xenopus lae	Aah70854 xenopus l	Q9gyz0 strongyloce
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عد	Query Match	99.5	99.5	83.4	56.5	56.5	55.5	55.5	55.5	55.2	55.0	54.9	36.5	27.2	24.4	24.4	23.8	23.7	23.7	23.6	23.6	23.5	23.3	23.3	23.1	22.9	22.6	22.4	22.4	22.4	22.4	22.4
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ALIGNMENTS

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ng prote ; Butele	Yonemura S. is localiz	Mura M., one	us.242603899; le J.G., .m., Schuler C.F., Bhat N. (J., Heleh F. M., Hong L., T.L., Scheet (Ci P., Mullah (R.D., Mu
PRT; 665 AA. ed) sequence update) annotation update) (Kinesin-like DNA-binding protein) KID; si Craniata; Vertebrata; Buteleostomis; Catarrhini; Hominidae; Homo.		Adati N., Matsumura i close to	TISSUE=ERRIN, and Lung; TISSUE=ERRIN, and Lung; TISSUE=ERRIN, and Lung; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.R. Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonahdo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy Broak S.A., Mekan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanch Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schwitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I. Skalska U., Smailus D.E., "Generation and initial analysis of more than 15,000 full-length
665 Au update on updai -like Di ata; Ve:	yoshima ing prof	C., T.,	DOI=10.1 Duse L.H. C. L., She C. H., Sch M. K., Sch M. K., Cch M. K., Mal M. K., Mal M. M. M
PRT; 665 AA. ed) sequence update) annotation update) (Kineain-like DNA KID; AID; a; Craniata; Verte	9929; A., To to T.; NA bind	0757; .Q., Ko , Ikeucl a K.K.; AZ are	77932; 1 A., Grow Magner uetow K refer to the former in th
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	[1] SEQUENCE FROM N.A. MEDLINE=56174806; PubMed=8599929; Tokai N., Fujimoto-Nishiyama A., Toyoshima Y., Tsukita S., Inoue J., Yamamoto T.; "Kid, a novel kinesin-like DNA binding protein chromosomes and the mitotic spindle.";	12) ESGUERICE FROM N.A. TISSUE-Lymphocytoblastoma; MEDLINE-99009323; Wubmed-9790757; MEDLINE-99009323; Wubmed-9790757; SONG J., Murakami H., Yang Z.Q., Koga Geltinger C., Saito-Ohara F., Ikeuchi Kanazawa I., Sun K., Yokoyama K.K.; "Human genes for KNSL4 and MAZ are loc chromosome 16pl.l."; Genomics 52:374-377 (1998).	TISSUEBRAIN, and Lung; TISSUE=Brain, and Lung; STAGUE=21388257; PubMed=12477932; DOI- Strausberg R.L., Feingold E.A., Grouse Klausner R.D., Collins F.S., Wagner L., Alteroull S.F., Zeeberg B., Buetow K.H., Hopkins R.F., Jordan H., Moore T., Max Diatchenko L., Marusina K., Farmer A.A. Stapleton M., Soares M.B., Bonaldo M.F. Brownstein M.J., Usdin T.B., Toshiyuki Raha S.S., Loquellano N.A., Peters G.J. Broak S.A., McEwan P.C., Hale S., Garcy Villalon D.K., Muzny D.M., Sodergren E. Fahey J., Helton E., Ketteman M., Madar Whiting M., Madan A., Young A.C., Shevo Blakesley R.W., Touchman J.W., Green E. Rodriguez A.C., Grimwood J., Schmutz J. Butterfield Y.S.N., Krzywinski M.I., Sk Schnerch A., Schein J.E., Jones S.J.M., "Generation and initial analysis of mox
œ ,	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=96174806; Tokai N., Fujimoto Tsukita S., Inoue "Kid, a novel kine chromosomes and the chromosomes and the	12) SEQUENCE FROM N.A. SEQUELLYmphocytol WEDLINE=99009323; SONG J., Murakami, Geltinger C., Sail Geltinger E., Sail Human genes for I "Human genes for I chromosome l6pl1.; Chromosome l6pl1.;	SEQUENCE FROM N.A TISSUE=Brain, and WEDLINE=22388257; WEDLINE=22388257; WEDLINES R.L., Control of the second of th
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APASAGOKLSPLOKLISSMDPAMLERLISLDRILASQGSQ
-> SSSICLEFETQPPTEAKAWWTRPCGAPPQLGPSACLPGE
P (in Ref. 2)
                                     Pubmed=11146551; DDI=10.1038/si.onc.1204002;

Rubmed=11146551; DDI=10.1038/si.onc.1204002;

Rocmani A., Bruzzoni-Glovanelli H., Fellous A., Gisselbrecht S.,

Varin-Blank N., Calvo F.;

"SIAH-1 interacts with alpha-tubulin and degrades the kinesin Kid by

"The proceasone pathway during mitosis.";

Oncogene 19:5997-6006(2000).

-I- FUNCTION: Kinesin family that is involved in spindle formation and

microtubules and to DNA.

-I- SUBCELLULAR LOCATION: Nuclear.

-I- PTW. Ubiquitinated, mediated by SIAH1 and leading to its

subsequent proceasonal degradation (Probable).

-I- SIMILARITY: Belongs to the kinesin-like protein family.
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GG; GO:0003677; F:DNA binding; TAS.

RG; GO:0003677; F:DNA binding; TAS.

RG; GO:0003677; F:DNA binding; TAS.

RG; GO:000377; F:DNA binding; TAS.

RG; GO:0000377; F:DNA binding; TAS.

RG; GO:0000377; F:DNA binding; TAS.

RICETPO; IPRO10583; HHH 1.

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RIMERPO; RRO10594; RuvA 2 - 1ike.

RRIMER; RRO10594; RICE; 1.

RAMART; SMO129; KINESIN HEAVY.

RAMART; SMO129; KINESIN HEAVY.

REAGITE; PSSO1067; KINESIN MOTOR DOMAINI; 1.

RROSITE; PSSO1067; KINESIN MOTOR DOMAINI; 1.

RROSITE; PSSO1067; KINESIN MOTOR DOMAINI; 1.

WATP-binding; Colled coil; DNA-binding; Microtubule; Motor protein; Modern Proventy.

M. NOL-lear protein; Ubl. Conjugation.
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AGOPRATWGDPAGSHGPPAAHKGGGCRGPAMG (in Ref.
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HCPTMLR -> RTIVPQCSG (in Ref. 2)
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Pred. No. 2.1e-159;
....rrhes 0; Indels
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ATP (Potential).
Missing (in Ref. 2).
S -> KV (in Ref. 2).
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Conservative 0; Mismatches
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EMBL; AB017333; BAA33063.1; --
EMBL; AB017333; BAA33063.1; JOINED.
EMBL; AB01734; BAA33063.1; JOINED.
EMBL; BC004352; AAH04352.1; --
EMBL; BC028155; AAH28155.1; --
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Gaps ; 0 3 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS 2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS

Best Local Similarity Matches 510; Conserv

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123 SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 182
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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koulnine N., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Koundinya M., Rapher A., Phelan M., Farmer A., "Cloning of human full-length CDSs in BD Creator (TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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EMBL, BT007259; AAP35923.1; -.
SEQUENCE 665 AA; 73261 MW; C6C0AC96741DD387 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
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SEQUENCE FROM N.A.

STRAIN=FVBAN TISSUE=Ammmary tumor. C3;

MEDLINE=2238257; PubMed=1247932;

MEDLINE=2238257; PubMed=1247932;

A Itachul S.F., Zeeberg B. E., Grouse L.H., Derge J.G.,

A Itachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,

A Itachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Adramson R.D., Millahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                  RSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL 302
                                                                                                    301
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                                                                                                                                   EKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQ
                   AARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPAS
                                                                                                                                                                                                                           ASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLE
                                                                                                                                                                                                                                                                                               ASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinge; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=FVB/N; TISSUE=Mammary tumor. C3; Strausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kinesin family member 22.
Name-Kif22;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      660 AA
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GO; GO:0000785; C:chromatin; IDA.
GO; GO:0005819; C:spindle; IDA.
InterPro; IPR003583; HHH_1.
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HSSP; P33173; 115S.
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 183
                                                                  243
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GPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLD 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 HAVLLVKVDQRERLTPFRQREGKLYLIDLAGSEDNRRTGNQGIRLKESGAINTSLFVLGK 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVINRPFTNESLQPHALAPVKLSQKELLGPSEAKKAKGPEEESTGSPESTAAPASASQKL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLOKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVBEKDLEIERLK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 TOORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 TCPQRREMASAT----SGPGRC-VSKGGLGRRPPLARVRVAVRLRPFMDGETEAKELPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 RAIDSCSLEVANWKKYQETLKYQFDAFYGEKSTQQEVYVGSVQPILRHLLEGQNASVLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GPTGAGKTHTMLGSPEQPGVIPRALMDLLQLAREESAEGRPWDVSVAMSYLEIYQEKVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRS
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TISSUB=Embryo;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                o
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                                                                                                                                                                                                                                                                                                                                                   Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels
InterPro; IPR001752; kinesin_motor.
InterPro; IPR01094; RuvA_2_like.
Pfam; PF00255; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN1; 1.
STOPHOSING; MICTOLOULD: MOTOR_DOMAIN1; 1.
SEQUENCE 660 AA; 73189 MW; AA8B99477BC49B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein MGC75575.
                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                   83.4%; Score 2158.5; DB 2
84.8%; Pred. No. 3.8e-132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 TKOKELEAKMLAOKA---EEKENHCPTM 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     639
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121

67 61 181

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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soarsen M.B., Bonaldo M.E., Carainci P., Scheetz T.E., Brapleton M., Soarsen M.B., Bonaldo M.E., Carainci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mitting M., Madan A., Xoung A.C., Shevchenko Y., Bouffard G.G., Antiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Schwutz J., Dickson M.C., Stalsky R.W., Schmutz J., Myers R.M., Butcerfield Y.S., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 EGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQK--LSSMDPAMLERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 MKRPRE----EAETAAGSRQRKKSKTDSTESSPNTSMDAASKRKINLAALDPAVVERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLDRILLASQGSQGAPILSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAB-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 639 AA; 71390 MW; P5664F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.5%; Score 1463; DB 2; Length 6 larity 60.3%; Pred. No. 7.8e-87; Conservative 79; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                            Klein S., Straubberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG3896; AAHG3896.1; -
InterPro; IPR01752; Kinesin motor.
InterPro; IPR010994; RuvA_2_like.
                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                     sednences.
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Matches 292; Conserv
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TISSUB-Embryo,

RY STGUENDER TO.

RY CARGED TO.

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REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

RETARREBERGY.

RETARREBERGY.

RA Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jecherg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Modin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S. Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Hakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Blakesley R.W., Bulkesley R.W., Bulkerfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

RA Gones S.J., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RALMDLLQLTREE--GAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 EGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 TGKLYLIDLAGSEDNRRTGNQGIRLKESGAINSSLFTLSKVVDALNQGLPRIPYRDSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QFDAFYGDSATQREIYMGSVCHILPHLLIGQNASVFAYGPTGAGKTHTMLGNPSQPGVIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                             Xenopus tropicalis, (Western clawed frog) (Silurana tropicalis).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%; Score 1463; DB 2; Length 6 60.3%; Pred. No. 7.8e-87; ive 79; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC1053896; AAH63896.1; -.
Hypothetical protein protein
SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sci. U.S.A. 99:16899-16903(2002).
                                     25-MAR-2004 (TrEMBLrel. 27, Created)
25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Ż
                                                                                    Hypothetical protein MGC75575.
MGC75575.
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Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.
  PRELIMINARY;
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=8364;
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AAH63896
AAH63896;
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WEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-228828 R.L., Felingold B.A., Grouse L.H., Derge J.G.,

MEDLINE-228828 R.L., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

MEDLINE-228828 R.L., Moore T., Max S.I., Wang J., Haich F.,

MEDLINE-228828 R.L., Parmer A.A., Rubin G.M., Hong L.,

MEDLINE-22882 R.L., Moore T., Max S.L., Wang C.,

MEDRING S.A., Mockenan K.J., Malek J.A., Guarathe P.H.,

MILLION D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

MILLION D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

MILLION D.K., Muzny D.M., Gaergren E.J., Lu X., Gibbs R.A.,

MILLION M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILLION M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MARTING M., Marra M.A.,

MERSPANNISKI M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,

JONES S.J., Marra M.A.;

Medneration and initial analysis of more than 15,000 full-length human
SEQUENCE FROM N.A.
MEDLINE=20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
                                                       446 SLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAE-E
                                       388 KLSQKELLGPPEAKRARGPEEEFIGSPEPMAAPASASQKLSPLQK--LSSMDPAMLERLL
                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Xkid, a chromokinesin required for chromosome alignment on the
                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Kinesin (Hypothetical protein) (Chromokinesin Xkid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequences.
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metaphase plate.";
Cell 102:425-435(2000).
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                                                                                                                                          KENH 508
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                                                                                                                                                                   KSTN 482
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
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Q91869;
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149 PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 206
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17 RVSMLDQHKKSSCARVRVAVRLRPYMDEKDEAKATTVCVRGLDSQSLEIVNWRNQLETMQ 76
                                                                                                                TISSUE=Blastula;
MEDLINE=99340303; PubMed=10411507;
Zou H., McGarry T.J., Bernal T., Kirschner M.W.;
"Identification of a vertebrate sister-chromatid separation inhibitor involved in transformation and tumorigenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Funabiki H., Murray A.W.;
"The Xenopus chromokinesin Xkid is essential for metaphase chromosome
alignment and must be degraded to allow anaphase chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
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PROSITE; PS0061; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 651 AA; 73065 MW; C2ABAS61C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.5%; Score 1438; DB 2; Length 65
60.1%; Pred. No. 3.4e-85;
ive 80; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Blastula; McGarry T.J., Bernal T., Funabiki H., Kirschner M.W.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
   R.;
to the EMBL/GenBank/DDBJ databages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0005677; F:ATP binding; IEA.
GO; GO:000377; F:BNA binding; IEA.
GO; GO:0003774; F:mctor activity; IEA.
InterPro; IPR010996; DNApol B.N.like.
InterPro; IPR003583; HHH 1.
InterPro; IPR001752; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20419288; PubMed=10966104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ249840; CAB71798.1; --
EMBL; BC070549; AAH70549.1; --
EMBL; AF267849; AAF82563.1; --
HSSP; P33173; 1155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00225, Kinesin, 1. –
PRINTS, PR00380, KINESINHEAVY.
SWART; SW0078; HhH1; 2.
SWART; SW00129, KISC; 1.
                                                                                                                                                                                                                                                                   Science 285:418-422(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 102:411-424 (2000)
Klein S., Strausberg
Submitted (MAY-2004)
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Atlasner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Atlachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bara N.K.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McKwan P.J., McKernan K.J., Maake J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A.N., Rodrigues S., Sanchez A.,
Mylting M., Madan A., Young A. Schwerchenko Y., Bouffard G.G.,
Mylting M., Madan A., Young A. Schwerchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schwerchenko Y., Bouffard G.G.,
A Jones S.J., Marra M.A.,
T., "Generation and initial analysis of more than 15,000 full-length human
                      377 MKRPREETGHIAGSQKRKKSKNDSTE--SSPN-SSMDTAGKQKLN----LATLDPAVVER 429
                                                                                                443
                                                                          LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAE 503
VKLSQKE---LLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLER
                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.5%; Score 143%; DB 2; Length 651; 60.1%; Pred. No. 3.4e-85; ive 80; Mismatches 100; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070549; AAH70549.1; -.
Hypothetical protein.
SEQUENCE 651 AA; 73065 MW; C2ABA561C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                                                13-MAX-2004 (TrEMBLrel. 27, Created)
13-MAX-2004 (TrEMBLrel. 27, Last sequence update)
13-MAX-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                              651 AA
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus; Xenopus
NCBI_TaxID=8355;
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                                                                                                                                                             504 -EKENH 508
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TISSUE=Embryo
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Gaps

Best Local Similarity 60.1 Matches 292; Conservative

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Punabiki H., Murray A.W.;

"The Xenopus chromokinesin Xkid is essential for metaphase chromosome alignment and must be degraded to allow anaphase chromosome irr punabiki H., Murray A.W.;

"The Xenopus chromokinesin Xkid is essential for metaphase chromosome irr purposent and must be degraded to allow anaphase chromosome irr purposent.";

"Cell 102:411-424(2000).

"EMBL; AF267850; AAF82564.1; -.

"REML; AF267850; AAF82564.1; -.

"REML; AF3785; Pintracellular; IEA.

"GO; GO:0005522; C:microtubule associated complex; IEA.

"GO; GO:0003774; F:DNA binding; IEA.

"REML; PRO10552; Kinesin motor.

"REML; PRO1752; Kinesin motor.

"REML; PRO1752; Kinesin motor.

"REML; PRO1752; Kinesin motor.
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                                                                                                                                                                                        RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLEIANWRNHQETLK
               89 YORDAFYGERSTOODIYAGSYOPILRHILLEGONASYLAYGPTGAGKTHTMLGSPEOPGVI
                                                                       149 PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                 LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651 AA.
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PRINTS, SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
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Xenopus laevis (African clawed frog).
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MEDLINE=20419288; PubMed=10966104;
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
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Best Local Similarity 59.4%;
Matches 287; Conservative 8
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Cell 102:425-435(2000)
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NCBI_TaxID=8355;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin family member 22 (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                       Length 651;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BC043733; AAH43733.1; -.
RSP: P3173; II5S.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:microtubule associated complex; IEA.
RG; GO:0005524; F:ATP binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
RG; GO:0003774; F:DNA binding; IEA.
R InterPro; IPR010996; DNApol_B N_like.
R InterPro; IPR0103583; HHH_1.
R InterPro; IPR001752; Kinesin_motor.
                                                                                                        ; Pred. No. 4e-85;
80; Mismatches 100; Indels
                                                                                     DB 2;
                          r protein.
C4EF79801E603C13
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1. ATP-binding; Microtubule; Motor protein. SEQUENCE 651 AA; 73091 MW; C4EF79801E60:
                                                                                   55.5%; Score 1437; 60.1%; Pred. No. 4e
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NCBI_TaxID=8355;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MEDLINE=20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Xkid, a chromokinesin required for chromosome alignment
                                                                                                                 Length
                                                                           74538 MW; 3B98B5F3C12C9C22 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                 1.6e-84;
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; PROSITE; PS50067; KINESIN MOTOR DOMAIN2; ATP-binding; Microtubule; Motor protein.
                                                                                                               Score 1428;
Pred. No. 1.
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285;
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                                                                                                                                                                                                                                                                                                              267 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 YQFDAFYGERSTQQDIYAGSYQPILRHLLEGQNASYLAYGPTGAGKTHTMLGSPEQPGVI
                                                                                                                                                                                                                                                                                                                                           LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                      8
                                                                                                                                                                                    Length 650;
                                                                                                                                                                                  55.0%; Score 1423; DB 2; Length 6
59.4%; Pred. No. 3.2e-84;
ive 81; Mismatches 107; Indels
                                                                                                                                      PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor Protein.
SEQUENCE 650 AA; 73027 MW; EA8415BC4B9B0F4A CRC64;
  HSSP; P3377; 1155.

GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:intracellular; IEA.
GO; GO:0005875; C:intracellular; IEA.
GO; GO:000577; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
INTERPO: IPR010996; DNAPOL B. I.ike.
InterPro; IPR010996; DNAPOL B. I.ike.
InterPro; IPR001752; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631 AA.
                                                                                                 Pfam, PF00225; Kinesin, 1.—
PRINTS, PR003090; KINESINHEAVY.
SMART; SM00278; HHH1; 2.
SWART; SM00129; KISC; 1.
                                                                                                                                                                                               Best Local Similarity 59.49
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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NCBI_TaxID=8355;
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Attausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhar N.K.,
Altschul S.F., Joederg B. Buercow K.H., Schaefer C.F., Haise F.
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,
RA Raha S.S., Loquellano N.B., Proshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
Rahes J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Richards R.R., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Gones S.J., Marra M.A.;
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AKVRVAVRLRPYMEEKEEDKVPTACVRGLDSHSLEIVNWRNQLETMQYQFDAFYGDSASQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 -EEGARGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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PRINTS; PR00380; KINESINHEAVY.
SMART; SW00129; KISS; 1.
PROSITE; PS00411; KINESIN MOTOR_DOWAIN1; 1.
PROSITE; PS5067; KINESIN MOTOR_DOWAIN1; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 631 AA; 71084 MW; 11E8C9AB86EBD3F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073177; A4473177; A4473177; InterPro; IPR01752; Kinesin motor. InterPro; IPR010994; RuvA_2_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.9%; Score 1422; DB 2;
ilarity 60.6%; Pred. No. 3.6e-84;
Conservative 78; Mismatches 99;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.
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SEQUENCE
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Best Local &
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SILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPE 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGGQNA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS 61
                371 SRQRKKSKTDSTESSPNSSMESTGKRKIN----LASLDSAVVERLLKIDKILTEKGKKEA
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99425270; PubMed=10493829; Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Caodon V.P., Kalush F., Branstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S., Bichler B.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q."; Genomics 60:255:308(1999).

EMBL: AC002101; AAC08709.1; -
                                                    400 AKRARGPEEEEIGSPEPMAAPASASOKLSPLOKLSSMDPAMLERLLSLDRLLASQGSQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
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                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-Mar-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kineain-like DNA binding protein (KID).
Name-A-328A3.2;
Name-A-328A3.2;
Butharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSS0667; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 198 AA; 21567 MW; 1A7FDA95B5A03B37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
InterPro; IICAPRO; IEA.
Ffam; PF00225; Kinesin, motor.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
36.5%; Score 946; DB 2; I
Best Local Similarity 100.0%; Pred. No. 7.6e-54;
Matches 183; Conservative 0; Mismatches 0;
                                                                                                                                                                                                             198
                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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 340
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148

PRT;

PRELIMINARY;

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RESULT 13 035232 ID 03523 AC 03523

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61 SGDLVIREDCRGNILIPGLTQKPITSFSDFEQHFLPASRNRAVGATRLNQRSSRSHAVLL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA
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                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97480723; PubMed=9339368;

MEDLINE=97480723; PubMed=9339368;

A Yang Z., Hanlon D.W., Marezalek J.R., Goldstein L.S.;

A Yang Z., Hanlon D.W., Marezalek J.R., Goldstein L.S.;

A Tidentification, partial characterization, and genetic mapping of kinesin-like procein genes in mouse.";

Genomics 45:123-131(1997).

EMBL, ARC13119; AAC39968.1; -.

RGO; GO:0000785; C:chromatin; IDA.

GO; GO:000785; C:chromatin; IDA.

GO; GO:0005819; C:spindle; IDA.

GO; GO:0005819; C:spindle; IDA.

RR Pfam; PF00225; Kinesin; 1.

PRINTS; PR00380; KINESINHEAVY.

RR SMART; SM00129; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.

ATP-binding; Microtubule; Motor protein.

T NON TER 148 148
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative kinesin-like DNA binding protein.
Name=OJ1281_H05.2;
OYYZA sativa (japonica cultivar-group).
Graya sativa (japonica cultivar-group).
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxIb=10090;
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Last sequence update)
Last annotation update)
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Pred. No. 3e-38;
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92.6%; Pred. No. Jer.
5; Mismatches
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                                                                                         (Fragment)
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01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2004 (TrEMBLrel. 26, Kinesin motor protein KIF22 Name=Kif22;
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Matches 137; Conservative
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171 QLKGLAWVPVRSLEEFHEIYSIGVQRRKVAHTGLNDVSSRSHAVLSIRITT-----DV 223
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AAT39162;

AAT39162;

O1-JUN-2004 (TrEMBLrel. 27, Created)
O1-JUN-2004 (TrEMBLrel. 27, Last sequence update)
O1-JUN-2004 (TrEMBLrel. 27, Last annotation update)
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al Similarity 36.1%; Score 633; DB 2; Length 58
al Similarity 36.1%; Pred. No. 8.5e-33;
166; Conservative 89; Mismatches 155; Indels
InterPro; IPR000445; HhH.

InterPro; IPR001752; Kinesin_motor.

Pfam; PF00623; HHH; 1.

Pfam; PF00025; Kinesin; 1.

PRINTS; PR001360; KIRSINHEAVY.

SMART; SM00129; KISC; 1.

PROSITE; PS00641; KINESIN MOTOR_DOMAIN; 1.

PROSITE; PS50067; KINESIN MOTOR_DOMAIN; 1.

ATP-binding; Microtubule; Motor_protein.

SEQUENCE 584 AA; 64124 MW; EP829G3AISF9190F CRC64;
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                                                                                              Gaps
                                                          20;
                                 Query Match
24.4%; Score 633; DB 2; Length 58
Best Local Similarity 36.1%; Pred. No. 8.5e-33;
Matches 166; Conservative 89; Mismatches 155; Indels
EMBL; AC117265; AAT39162.1; -.
SEQUENCE 584 AA; 64124 MW; EF829C3A15F9190F CRC64;
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 5, 2004, 18:34:11 ; Search time 51.8496 Seconds

(without alignments)

3839.562 Million cell updates/sec
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Title:

Perfect score: 1768
Sequence:

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O14807 homo sapien	Aap35923 homo sapi	Q991c7 mus musculu	Q6p3r1 xenopus tro	Aah63896 xenopus t	Q9i869 xenopus lae	Aah70549 xenopus 1	Q9i8k0 xenopus lae	Q7zyl5 xenopus lae		Q6gpg0 xenopus lae	O60845 homo sapien		Q61512 oryza sativ	9	Q817b8 arabidopsis	Q91z88 arabidopsis	Q8sqq9 encephalito		-		Q961h5 drosophila		P46867 drosophila	Q86vs5 homo sapien	Q8ni77 homo sapien	Q9h0f3 homo sapien	Q7rm16 plasmodium	Q8by99 mus musculu	Q8bz45 mus musculu	Q8b111 mus musculu
ID	KP22 HUMAN	AAP35923	Q99LC7	Q6P3R1	AAH63896	Q91869	AAH70549	Q918K0	Q7ZYL5	Q919A8	QGGPG0	060845	035232	Q6L512	AAT39162	Q8L7B8	Q9LZ88	Q8SQQ9	Q7RX60	Q7QDS6	Q86ZB6	Q961H5	QBN1X8	KL68 DROME	Q86V <u>S</u> 5	Q8N177	Q9H0F3	Q7RM16	Q8BY99	Q8BZ45	QBBLL1
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* Query Match Length	99.7	7.66	88.9	69.7	69.7	68.0	68.0	68.0	67.7	67.4	67.4	47.3	39.8	35.3	35.3	33.6	33.6	33.1	32.7	32.2	31.8	31.6	31.6	31.4	31.2	31.2	31.2	31.2	31.2	31.2	31.2
Score	1763	1763	1572.5	1232	1232	1202.5	1202.5	1201.5	1197.5	1192.5	1191.5	836	704	623.5	623.5	594.5	594.5	584.5	578	568.5	563	559.5	559	555.5	552.5	552.5	552.5	552	551.5	551.5	551.5
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ALIGNMENTS

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AAP35923;
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APASASOKLSPLOKLSSMDPAMLERLLSLDRLLASQGSQ
-> SSSLCLPETQPPTEAKAAWTRPCGAPPQLGPSACLPGE
P (in Ref. 2).
ENHCPTMLR -> RTIVPQCSG (in Ref. 2).
CGCOAC96741DD387 CRC64;
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Missing (in Ref. 2).
S -> KV (in Ref. 2).
HTMLGSPROPGVIPRALMDLLQLTREEGAEGRPWA -> TH
AGQPRATWGDPAGSHGPPAAHKGGGCRGPAMG (in Ref.
                                  Number 1146551; DOI=10.1038/8j.onc.1204002;

Retmand A., Bruzzoni-Giovanelli H., Fellous A., Gisselbrecht S., Germani A., Bruzzoni-Giovanelli H., Fellous A., Gisselbrecht S., Germani A., Bruzzoni-Giovanelli H., Fellous A., Gisselbrecht S., A Varin-Blank N., Calvo F.;

"SIAH-1 interacts with alpha-tubulin and degrades the kinesin Kid by T the proteasone pathway during mitosis.";

"Oncogene 19:5997-6006(2000).

"I PUNCTION: Kinesin family that is involved in spindle formation and the movements of chromsomes during mitosis and meiosis. Binds to microtubules and to DNA.

"SUBCELLULAR LOCATION: Nuclear."

"I SUBCELLULAR LOCATION: Nuclear."

"I SUBCELLULAR LOCATION: Mediated by SIAH1 and leading to its subsequent proteasomal degradation (Probable).

"I SIMILARITY: Belongs to the kinesin-like protein family.
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; HhH; 2.
SMART; SM00129; KISC; 1.
PROSTIE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSTIE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Colled coil; DNA-binding; Microtubule; Motor protein;
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99.7%; Score 1763; DB 1; Length 665;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 345; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coiled coil (Potential)
ATP (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005634; C:nucleus; TAS.
GO:0003677; F:DNA binding; TAS.
GO:0003777; F:microtubule motor activity; TAS.
GO:0007067; P:mitogis; TAS.
        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinesin-motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001583; HHH 1.
InterPro; IPR001752; kinesin motor.
InterPro; IPR010994; RuvA_2_11ke.
                                                                                                                                                                                                                                                                                                                                                                             EMBL, AB017335, BAA33063.1; --
EMBL, AB01733, BAA33063.1; JOINED.
EMBL, AB017334, BAA33063.1; JOINED.
EMBL, BC004352, AAH04352.1; --
EMBL, BC028155, AAH28155.1; --
HSSP, P33173; 1155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 603213; -.
GO; GO:0000776; C:kinetochore; TAS.
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73262 MW;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB017430; BAA33019.2; -.
 cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew, HGNC:6391, KIF22.
MIM, 603213, -.
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DOMAIN 40 29
DOMAIN 465 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LKYQPDAFYGERSTQQDIYAGSVQPILRHILEGQNASVLAYGPTGAGKTHTWLGSPEQPG 121
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                                                                                                                                                                                                                                                                  266 REGRLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 325
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LKYOFDAFYGERSTQQDIYAGSYQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPBQPG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 GRCRLSKIGATRRPPFARVRVAVRLRPFVDGTAGASDFPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 VIPRALMDILQLIREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                    VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                             REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                           SEQUENCE FROM N.A. Kalnines L., Bisenstein S., Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector."; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2003) to the EMBL; BT007259; AAP35923.1; -. SEQUENCE 665 AA; 73261 MW; C6C0AC96741DD387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O2-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 99.7%; Score 1763; DB 2; I Local Similarity 100.0%; Pred. No. 1.2e-128; hes 345; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Attaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altachul S.P., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.P., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,
And Straubberg R.P., Jordan H., Moore T., Max J.L., Mang J., Hsich F.,
Astapleron M., Soares M.B., Bonaldo M.F., Casrainci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan R.J., Markarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                       200
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                                                                                                                                                                                                                                                              REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ñ
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SMART; SM01129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR_DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
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                                                                                                                                                                                                                                                                                                                                                          302 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                            TRILQDSLGGSAHSILIANIAPERRFYQDTISALNFTARSKEVIN 365
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BE063896; AAH63989; Kineein motor.
InterPro; IPR001752; Kineein motor.
InterPro; IPR010994; RuvA-2_like.
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein MGC75575.
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68.6%; Pred. No. 2.8e-87;
iive 53; Mismatches 53;
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MEDLINE=22388257; PubMed=12477932;
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Best Local Similarity 68.6'
Matches 236; Conservative
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NCBI_TaxID=8364;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altasner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahesley S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
McKrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
The Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 LKYQFDAFYGEKSTQQEVYVGSVQP1LRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003427; AAH03427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO04il; KINESIN MOTOR DOMAINI; 1.
PROSITE; PSSO67; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor_protein.
SEQUENCE 660 AA; 73189 MW; AA8B99477BC49B3C CRC64;
                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                               660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:109233; Kif22.
GO; GO:0000785; C:chromatin; IDA.
GO; GO:0005819; C:spindle; IDA.
InterPro; IPR001583; HHH 1:
InterPro; IPR001752; kineein motor.
InterPro; IPR010994; RuvA_2_Iike.
Pfam; PF00225; Kineein; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                           Created)
                                                                                            PRT;
                                                                                                                                                 (TrEMBLrel. 17, C
(TrEMBLrel. 17, L
(TrEMBLrel. 26, L
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                                                                                                                                                                                                                                                       Kinesin family member 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.
                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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ses 305; Conserv
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                                                                                                                                                        01-JUN-2001
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Length

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01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 05-JUL-2004 (TrEMBLrel. 27,
                     68.68;
                        Best Local Similarity 68.6
Matches 236; Conservative
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Cell 102:425-435(2000).
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NCBI_TaxID=8355;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                 RALMDLLQLTREE--GAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNIL 182
                                                                                                                                                                                                                                                            OPDAFYGERSTOQDIYAGSVQPILRHLLEGONASVLAYGPTGAGKTHTMLGSPEQPGVIP 124
                                                                                                                                                           64
                                                                                63
                                                                                                                                                                                                                                                                                                                                     IPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                        EGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                                           RLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063896; AAH63896.1; -.
Hypothetical protein.
SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN
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Last annotation update)
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SEQUENCE FROM N.A.
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X. Straubberg R.L., Feligold B.A., Grouse L.H., Derge J.G., Schuler G.D.,

X. Straubberg R.L., Feligold B.A., Grouse L.H., Schamen C.M., Schuler G.D.,

X. Rlausener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X. Rlausener R.D., Collins F.S., Mactow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Antechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worden P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Wolfley K.C., Hale S., Garcia A.N., Gabbs R.A.,

X. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X. Halton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M. M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Razywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Razywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Razywinski M.I., Sana M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                         QFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIP 124
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SEQUENCE FROM N.A.
MEDILINE-20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
                                                                                                                                                                                                                                                                                                                                                                                        RALMDLLQLTREE--GAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 ECKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 IPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQR
                                                                                                                              5 RLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQETLKY
                                                                                                                                                                    |:| : ::| |||||||||||::|
RVSILDQHKKPSSARVRVAVRLRPYMEKEDEKAPAACVRGLDSQSLEIVNWRNQLETMOY
                                                                    Gaps
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                                                                       23;
; Score 1232; DB 2;
; Pred. No. 2.8e-87;
53; Mismatches 53;
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MEDLINE=223825;

MEDLINE=223825;

MEDLINE=223825;

MEDLINE=223825;

MEDLINE=238825;

MEDLINE=238825;

MALSCHOL S. Pelngold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buercw K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Heish F.,

Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Milalon D.K., Marzy D.M., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                         137 PRAVRDLLQMSRTAASAPENENWTYTINMSYVEIYQEKVMDLLEPKNKDLPIREDKDHNI 196
                                                                                                                                                                                                   257 LTGKLYLIDLAGSEDNRRTGNQGIRLKESGAINSSLFTLSKVVDALNGGLPRIPYRDSKL 316
                                                          LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                  242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL
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Kanopus laevis (African clawed frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22341122, PubMed=12454917,
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
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67.8%; Pred. No. 5.7e-85;
ive 52; Mismatches 56; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070549; AAH70549.1; -.
Hypothetical protein
SEQUENCE 651 AA; 73065 MW; C2ABAS61C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                     317 TRLLQDSLGGSAHSVMITNIAPEQTYYFDTLTALNFAAKSKQIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-2004 (TrEMBLrel. 27, Created)
13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
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Best Local Similarity 67.8
Matches 234; Conservative
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AAH70549;
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17 RVSMLDQHKKSSCARVRVAVRLRPYMDEKDEAKATTVCVRGLDSQSLEIVNWRNQLETWQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zou H., McGarry T.J., Bernal T., Kirschner M.W.; "Identification of a vertebrate sister-chromatid separation inhibitor involved in transformation and tumorigenesis."; Science 285:418-422(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Funabiki H., Murray A.W.; "The Xenopus chromosin sesential for metaphase chromosome alignment and must be degraded to allow anaphase chromosome
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                                                                                                                                              Klein S.L., Strausberg R.L., Wagner L.; Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                    "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 651 AA; 73065 MW; C2ABA561C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 651;
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
REBL; AJZ49840; CAB71798.1; -.
REBL; AJZ49840; CAB71798.1; -.
REBL; AF267849; AAH70549.1; -.
REBL; AF267849; AAH70549.1; -.
REBL; AJZ49840; Calitracellular; IEA.
GG; GG:0005522; C:intracellular; IEA.
GG; GG:0005524; F:ATP binding; IEA.
GG; GG:0003577; F:DNA binding; IEA.
GG; GG:000377; F:DNA binding; IEA.
GG; GG:000377; F:DNA binding; IEA.
RG; GG:000377; F:DNA binding; IEA.
RINCEPPO; IPR003583; HHH-1.
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                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001752; kinesin motor.
                                                                                                          TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Blastula;
MEDLINE=99340303; PubMed=10411507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20419288; PubMed=10966104;
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PRINTS: PRO03480; KINESINHEAVY.
SMART; SM00278; HHH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002).
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Submitted (MAY-2004) to
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TISSUE=Blastula;
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                                                                                 SEQUENCE
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Funabiki H., Murray A.W.;
"The Xenopus chromokinesin Xkid is essential for metaphase chromosome
alignment and must be degraded to allow anaphase chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                  242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
   RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLBIANWRNHQETLK
                                                                                                                    YQPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
                                                                                                                                                                                                                                                                            LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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GO: GO: 0005875; C: microtubule associated complex; IEA.
GO: GO: 0005875; C: microtubule associated complex; IEA.
GO: GO: 0005577; F: DAA binding; IEA.
GO: GO: 0003777; F: DAA binding; IEA.
InterPro; IPR010996; DNApol B.N.like.
InterPro; IPR010996; MAPOl B.N.like.
InterPro; IPR0101752; Kinesin; 1.
REANTYS; RR0380; KINESINHEAVY.
SWART; SW00279; HAH1; 2.
SWART; SW00279; KISC; 1.
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 651 AA; 73091 MW; C4EF79801E603C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
11-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Chromokinesin Xkid.
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movement:";
Cell 102:411-424(2000).
EMBL; AF267850; AAF82564.1; -.
HSSP; P33173; 115S.
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Matches 234; Conservative
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 123
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                                                                                                                  LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                  242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                       PRALMDLLQLTREEGA - - EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
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YOFDAFYGERSTQQDIYAGSYQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                   57; Indels
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO43733; AAH43733.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complex; IEA
                                                                                                                                                                                                                                                                                                                                                                    01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07N-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin family member 22 (Fragment).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 67.7%; Score 1197.5; DB Local Similarity 67.5%; Pred. No. 1.4e-84; Les 213; Conservative 52; Mismatches 57
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256
                                                                   182 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                      242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR_DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
                                                                                                       302 TRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073177; AAH73177.1; -.
InterPro; IPR010752; kinesin motor.
InterPro; IPR010994; RuvA 2 like.
Pfam; PF00225; Kinesin; 1.
                                                                                                                       317 TRLLQDSLGGSAHSVMITNIAPEQTYYFDTLTALNFAAKSKQIIN
                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                631 AA
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
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05-JUL-2004
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Q6GPG0
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                                                                                                   242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOFDAFYGERSTOQDIYAGSVQPILRHILEGQNASVLAYGPTGAGKTHTWLGSPEQPGVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRALMDLLQLTR--EEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                           TRILLODSIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                      58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS5067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 650 Aa; 73027 MW; EA84158C4B9B0F4A CRC64;
                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.4%; Score 1192.5; DB 3
llarity 67.5%; Pred. No. 3.4e-84;
Conservative 51; Mismatches 58.
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GO; GO:0005875; C:microtubule associated of GO:0005524; P:ATP binding; IEA.
GO; GO:0003677; P:DNA binding; IEA.
GO; GO:0003774; P:Motor activity; IEA.
THERPEO: IPR01099; DNADOL B. N. like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003583; HHH 1. — —
InterPro; IPR001752; Kinesin_motor.
Pfam; PP00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              metaphase plate.",
Cell 102:425-435(2000).
EMBL; AJZ49841; CAB71799.1; -.
HSSP; P33173; 1158.
                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Vernos I.;
                                                              210
                                                                                                                                                                                                                                                                                                            Name=kid;
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                                      182
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LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
                           86 LKYQPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 GKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. GKTHTMLGSPEQPGVIPRALMDLLQLARESABGRPWDVSVAMSYLEIYQEKVLDLLDPA
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name-CA1281 H05.2;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X EQUENCE FROM N.A.

X MEDLINE=9480723; PubMed=9339368;

A Yang Z., Hanlon D.W., Marszalek J.R., Goldetein L.S.;

Yang Z., Hanlon D.W., Marszalek J.R., Goldetein L.S.;

A Yang Z., Hanlon D.W., Marszalek J.R., Goldetein L.S.;

X Indentification, partial characterization, and genetic mapping of kinesin-11ke protein genes in mouse.";

Golomics 45:123-131(1997).

R RFMI, ARC13119; AAC3968.1; -.

R MGD; MGI:109233; Kif22.

R MGD; MGI:109233; Kif22.

RR GO; GO:0005819; C:chromatin; IDA.

RO; GO:0005819; C:chromatin; IDA.

RR GO; GO:0005819; C:chromatin; IDA.

RR PROSITE; PRO0129; KINESIN-MOTOR DOMAIN; 1.

RR SMART; SM00129; KINESIN-MOTOR DOMAIN; 1.

RR ATP-binding; Microtubile; Motor protein.
                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.8%; Score 704; DB 2; Length 148; 92.6%; Pred. No. 5.5e-47; tive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AA; 16596 MW; 0950C265C3B63EB7 CRC64;
                                                                                                               VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKV 184
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VKVDQRERLTPFRQREGKLYLIDLAGSE 148
                                                                                                                                                                                                                                                                                                                                Kinesin motor protein KIF22 (Fragment).
                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 137; Conservative
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NON TER
SEQUENCE
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EMBL; AC002301; AAC08709.1; -.

EMBL; AC002301; AAC08709.1; -.

RO; GO:0005524; F:MTP binding; IEA.

GO; GO:0005524; F:MTP binding; IEA.

GO; GO:0005774; F:mctor activity; IEA.

DR GO; GO:0005524; K:mesin, L.

SNART; SM00129; Kinssin, L.

SNART; SM00129; Kinssin, L.

SNART; SM00129; Kinssin, Motor Dowans; 1.

RPROSITE; PS50067; KINSIN MOTOR DOWANS; 1.
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                                                                                                                                                                                                                                                                                136 - EEGAEGRPWALSVTWSYLEIYQEKVLDILDPASGDLVIREDCRGNILIPGLSQKPISSF
                                                                                                                                                                                                                                                                                                                                                                                                                                            EDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAH
                                                                                                                                           195 ADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGS
                                                                                                                                                                                                                                                                                                                                                                                       18 ARVRVAVRLRPFVDGTAGASDP-PCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQ
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                                                                              Gaps
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin-like DNA binding protein (KID).
Name-A-328A3.2;
Name-A-328A3.2;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        DB 2; Length 631;
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                                     67.4%; Score 1191.5; DB 2; Length
69.6%; Pred. No. 3.9e-84;
iive 48; Mismatches 50; Indels
11E8C9AB86EBD3F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.3%; Score 836; DB 2; L
100.0%; Pred. No. 4.2e-57;
ive 0; Mismatches 0;
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    71084 MW;
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Matches 159; Conservative
                                            Query Match
Best Local Similarity 69.65
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O60845;
01-AUG-1998 (TrEMBLrel.
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SEQUENCE FROM N.A.
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RESULT 12

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Gaps

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Query Match

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23;

DB 2; Length 584;

57

181

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283

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58 ECYKLDAFFGQESRVCEIFDQEVSAVIPGIFEGTNATVFAYGATGSGKTYTMQGTEDLPG 117
                                                                                                                                                                                                                                                                                                       64 --YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
                                                                                                                                                                                                                                                      224 VKGKLNLIDLAGNEDNRRTCNEGIRLQESAKINQSLFALSNVISALNKKEPRIPYRESKL
                                                                                                                                                                                                                                6 LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
Chen Y.-L., Cheng. C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
Hsiung J:-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.,
"Oryza sativa BAC OJ1281 H05 genomic sequence.";
Submitted (JUN-2004) to The EMBL, GenBank/DDBJ databases.
EMBL, AC117265; AAT39162.1;
SEQUENCE 584 AA; 64124 MW; EF829C3A15F9190F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRILODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                            35.3%; Score 623.5; DB 2; Length 40.9%; Pred. No. 6.4e-40; ive 68; Mismatches 113; Indels
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                                                                                                                                                                                                   Conservative
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                                                                                                                                                                               Similarity
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                                                                                                                                                            Query Match
Best Local Simil
Matches 141, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
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                                                                                                                                            Leu H.-L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 LIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPFRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
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0/1281 H05.2.
0/1282 Fativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza sativa.
                                                              A Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
A Chow Y.-T., Chang S.-J., Chen H.-C., Chen S.-W., Chen T.-R.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-W., Chen T.-R.,
A Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Haiao S.-H.,
Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
I Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
I Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL, ACII1265, AAT39162.1, -
R InterPro; IPR010996; DNApol B.N.like.
R InterPro; IPR000445; HhH.
R InterPro; IPR00152; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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PROSITE; PSSO67; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor_protein.
SEQUENCE 584 AA; 64124 MW; EF829C3A15F9190F CRC64;
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         35.3%; Score 623.5; DB 2;
40.9%; Pred. No. 6.4e-40;
tive 68; Mismatches 113;
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SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                 Pfam; PF00633; HHH; 1.
Pfam; PF00225; Kinesin; 1.
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Matches 141; Conservative
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                                    NCBI_TaxID=39947;
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01-JUN-2004 (
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This rage blaink (uspto)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2004, 18:34:11; Search time 72.979 Seconds (without alignments) 3839.562 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-797-893-8 2472 1 MGRCRLSKIGATRRPPPARV.....LEAKMLAQKAEEKENHCPTM 487

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	014807 homo sapien	Aap35923 homo sapi	O991c7 mus musculu	Q6p3r1 xenopus tro	Aah63896 xenopus t	Q9i869 xenopus lae	Aah70549 xenopus 1	Q9i8k0 xenopus lae	Q7zyl5 xenopus lae						Aat39162 oryza sat	Q961h5 drosophila		Q91z88 arabidopsis			Q8sqq9 encephalito	Q7rx60 neurospora	Q7qds6 anopheles g	Q9fz77 arabidopsis		Q7qy55 giardia lam		Q91784 xenopus lae	Q6irm2 xenopus lae	Aah70854 xenopus l	Q9gyz0 strongyloce
SUMMARIES	ID	KF22 HUMAN	AAP35923	Q99LC7	Q6P3R1	AAH63896	091869	AAH70549	Q918K0	Q7ZYL5	Q919A8	QGGPG0	060845	035232	Q6L512	AAT39162	Q961H5	Q8L7B8	Q9LZ88	KL68 DROME	Q86ZB6	600880	Q7RX60	Q7QDS6	Q9FZ77	Q9VRK9	Q7QY55	Q7M624	KF4A XENLA	Q61RM2	AAH70854	Q9GYZ0
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	Query Match	99.8	99.8	86.1	59.2		58.2	58.2	58.1	57.8	57.6	57.5	33.8	28.5	25.6	25.6	24.9	24.8	24.8	24.8	24.7	24.6	24.4	24.4	24.2	24.0	23.6	23.5	23.4	23.4	23.4	23.4
	Score	2467	2467	2129.5	1463	1463	1438	1438	1437	1428	1423	1422	836	704	633	633	616	614	614	612	611.5	608.5	604	603.5	597.5	593	584.5	580.5	579.5	579.5	579.5	579
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Q8BZ45 Q8BLL1 Q91WD7 Q6DIN5 Q6PKB2 AAH0364 Q8FXN3 KF4A HUMAN Q8BY99 Q7ZUW9 Q9BT11 Q9BT11 Q8GXX7
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                       V -> A (in Ref. 2).
APASASQVIESPLOKLISMOPAMLERLLSLDRLLASQGSQ
-> SSLCLEPETQPPERKAMWTRPCGAPPQLGPSACLPGE
P (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinesin-motor.
Coiled coil (Potential).
ATP (Potential).
Missing (in Ref. 2).
S -> KV (in Ref. 2).
HTMLGSPEQPGVIPRALMDLIQLTREEGAEGRPWA -> TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS500671; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; DNA-binding; Microtubule; Motor protein;
Nuclear protein; Ubl conjugation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENHCPTMLR -> RIIVPOCSG (in Ref. C6C0AC96741DD387 CRC64;
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      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                 activity; TAS
                                                                                                                                                                                                                                                                                                                                              GO:0005634; C:nucleus; TAS.
GO:0003777; F:microtubule motor
GO:000707; F:microtubule motor
GO:0007067; P:mitosis; TAS.
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InterPro; IPR001752; kinesin motor.
InterPro; IPR010994; RuvA_2_like.
                                                                                                                                                                                                                                                         EMBL, AB017335; BAA33063.1; -. EMBL, AB017333; BAA33063.1; JOINED. EMBL, AB017334; BAA33063.1; JOINED.
                                                                                                                                                                                                                                                                                                                             MIM; 603213; -. GO; GO:0000776; C:kinetochore; TAS.
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                       EMBL; BC004352; AAH04352.1; -. EMBL; BC028155; AAH28155.1; -. HSSP; P33173; 1158.
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73262 MW;
                                                                                                                                                                                                                                                  EMBL; AB017430; BAA33019.2; -.
 mouse cDNA sequences.";
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665 AA;
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26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
27 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET

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145
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LIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQRERLAPFRQ 241
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                                                                                                                                                                                                                                                                         TRLLQDSLGGSAHS111ANIAPERRFYLDTVSALNPAARSKEVINRPFTNESLQPHALGP
                                                                                                                                                                                                                                                                                                                                                                                 386 VKLSQKELLGPPEAKRARGPEBEBIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                    122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinesin-like 4.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL: BT007259; AAP35923.1; -
SEQUENCE 665 AA; 73261 MW; C6C0AC96741DD387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
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Pred. No. 4.3e-153;
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Matches 486; Conservative 0; Mismatches
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NHCPTM 511
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al Similarity 86.3 422; Conservative
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Q6P3R1
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                  REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                  TRILQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                                                                                 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                                                                                                                          VKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                              LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAEEKE
LI PGLSQKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Straubberg R.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; B33173; 115S.
MGD; MGI:109233; Kif22.
MGD; MGI:09233; Kif22.
GO; GO:0000785; C:chromatin; IDA.
GO; GO:000785; C:chromatin; IDA.
InterPro; IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                660 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinesin family member 22.
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SEQUENCE FROM N.A.
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22 GRC-VSKGGLGRRPPLARVRVAVARLRPFMDGETEAKELPCVRAIDSCSLEVANWKKYQET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 LKYQFDAFYGEKSTQQEVYVGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 REGKLYLIDLAGSEDNRRTGNOGIRLKESGAINTSLFVLGKVVDALNOGLPRIPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 VIPRALMDLLQLAREESAEGRPWDVSVAMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKLSQKELLGPSEAKKAKGPEESTGSPESTAAPASASQKLSLLQKLSNMDPAMLENLLS
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=2238825;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausherg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 660;
                                                                                                                                                                                                                                                                                                                                             86.1%; Score 2129.5; DB 2; Length
86.3%; Pred. No. 5.5e-131;
ive 29; Mismatches 33; Indels
InterPro; IPR001752; kinesin motor.
InterPro; IPR010994; Ruva_2_like.
Pfam; PP00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; Hill; 2.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAINI; 1.
PROSITE; PS0067; KINESIN MOTOR_DOMAINZ; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 660 AA; 73189 MW; AA8B99477BC49B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheical protein MGC75575.
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Barusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKarnan R.J., Malek J.A., Gunaratne P.H.,
RA R., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rahina M., Wazuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Willalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
M. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Understion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAE-E 479
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PROSITE; PS5067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                               Klein S., Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC063986; AH618981 motor. InterPro; IPR01752; Kinesin motor. InterPro; IPR010994; RuvA_2_like. Pfam; PF00225; Kinesin; 1. PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISS. 1.
                                                                                                                                                                                                                                                                                Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Pred. No. 2.4e-87; 79; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 1463; DB 2; 60.3%; Pred. No. 2.4e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 60.39
Matches 292, Conservative
                                                                                                                                                                                                                                                                                                                    FROM N.A.
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TISSUB-Embryo;

XE SEQUENCE FROW N.A.

XET TISSUB-Embryo;

XE TISSUB-Embryo;

XE TISSUB-Embryo;

XE STATE SERVER R.L.;

XET TISSUB-Embryo;

XE STATE SERVER R.L.;

XE STATE SERVER R.R.;

XE STATE SERVER R.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPV 362
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                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Zenopus; Silurana.
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Klein S., Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
EMBL, BC063896, AAH63896.1; -.
Hypothetical protein.
SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 2.4e-87; 79; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 1463; DB 2; 60.3%; Pred. No. 2.4e-87;
                                                                 Last sequence update)
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639
                                                Created)
                                                                                                               Hypothetical protein MGC75575.
                                         25-MAR-2004 (TrEMBLrel. 27, 25-MAR-2004 (TrEMBLrel. 27, 25-MAR-2004 (TrEMBLrel. 27,
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  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
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TISSUE=Embryo;
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Brownstein M.J., Usdin T.B., Tonshiyuki S., Carninci P., Scheetz T.E.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Willalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Generation and initial analysis of more than 15,000 full-length human
418
                                                                                                                                                                                                                           478
                                                                                                                                                                         SLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAE-E 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
                                                                                                     364 MKRPRE----EAETAAGSRQRKKSKTDSTESSPNTSMDAASKRKINLAALDPAVVERLL
                                                                                                                                                                                                  363 KLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQK--LSSMDPAMLERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Xkid, a chromokinesin required for chromosome alignment on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Kinesin (Hypothetical protein) (Chromokinesin Xkid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                651 AA.
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MEDLINE=22388257; PubMed=12477932;
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MEDLINE=22341132; PubMed=12454917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metaphase plate.";
Cell 102:425-435(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
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SEQUENCE FROM N.A.
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Q91869;
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                                                                                           TISSUE-Blastula;
MEDLINE=99340303; PubWed=10411507;
Zou H., McGarry T.J., Bernal T., Kirschner M.W.;
"Identification of a vertebrate sister-chromatid separation inhibitor involved in transformation and tumorigenesis.";
Science 285:418-422(1999).
                                                                                                                                                                                                                                                                                                                                      Funabiki H., Murray A.W.;
"The Xenopus chromokinesin Xkid is essential for metaphase chromosome
alignment and must be degraded to allow anaphase chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLEIANWRNHQETLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS0067; KINESIM MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 651 AA; 73065 MW; C2ABA561C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McGarry T.J., Bernal T., Funabiki H., Kirschner M.W.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL249840; CAB17798.1;
EMBL; BC070549; AAH70549.1;
EMBL; AEC70549; AAH70549.1;
EMBL; AFS7849; AAH70549.1;
EMBL; AFS7849; AAH70549.1;
EMBL; AFS7879; AAH70549.1;
EMBL; AFS7879; AAH70549.1;
EMBL; AFS7879; AAH70549.1;
EMBL; AFS7879; AAH70549.1;
EMBC; GO:0005524; F:ATP binding; IEA.
GO; GO:0005774; F:DNA binding; IEA.
GO; GO:0003774; F:DNA binding; IEA.
GO; GO:0003774; F:DNA binding; IEA.
EMPC; IPR010996; DNApol B.N.like.
InterPro; IPR010996; DNApol B.N.like.
EMPC; AFR7879839; HHH.1.
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R.;
to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                  MEDLINE=20419288; PubMed=10966104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00225; Kinesin; 1
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Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 102:411-424 (2000)
Klein S., Strausberg
Submitted (MAY-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                             TISSUE=Blastula;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Blastula;
                                                                                                                                                                                                                                                                                                                                                                                                                  movement.";
                                                                                                                                                                                                                                                               SEQUENCE
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Best Local S
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                                                                                        LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAE 478
                                                                                                                   VKLSQKE---LLGPPEAKRARGPEEEEIGSPBPMAAPASASQKLSPLQKLSSMDPAMLER
                          AAH70549;
13-MAY-2004 (TrEMBLrel. 27, Created)
13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical devis (African clawed frog).
Bukaryota; Metazca; (Dordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070549; AAH70549.1; -.
Hypothetical protein.
SEQUENCE 651 AA; 73065 MW; C2ABA561C4C53C13 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                       651 AA
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NCBI_TaxID=8355;
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[2]
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Best Local Similarity 60.1<sup>1</sup>
Matches 292; Conservative
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                                                                                                                                                                                           -EKENH 483
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TISSUE=Embryo;
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                                                                        124 PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                            LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 241
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               TRILIODSIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
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                                                        64 YQFDAFYGERSTQQDIYAGSVQPILRHLLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLEIANWRNHQETLK
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoldea, Pipidae,
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(qell 102:411-424(2000).

(gell 102:411-424(2000).

(HSPE): PARF8256; AAF82564.1; -.

(HSPE): PARF8256; AAF82564.1; -.

(GO; GO:0005622; C:intracellular; IEA.

(GO; GO:0005875; C:intracellular; IEA.

(GO; GO:0003677; F:DNA binding; IEA.

(GO; GO:0003774; F:mortor activity; IEA.

(InterPro; IPR010996; DNApol_B_N_like.

(InterPro; IPR003583; HHH_1.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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MEDLINE=20419288; PubMed=10966104;
Funabiki H., Murray A.W.;
"The Xenopus chromokinesin Xkid is essential for alignment and must be degraded to allow anaphase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    651 AA.
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PRINTS; PR00380; KINESINHEAVY.
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SMART; SM00129; KISC; 1.
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Pfam; PF00225; Kinesin; 1
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metaphase plate.";
Cell 102:425-435(2000).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin family member 22 (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                          14;
                                                                                    651;
                                                                                58.1%; Score 1437; DB 2; Length 6 60.1%; Pred. No. 1.3e-85; ive 80; Mismatches 100; Indels
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; RC043733; AH443733.1; -.
HSSP; P33173; 11SS.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005525; C:microtubule associated complex; IEA.
GO; GO:0005777; F:ATP binding; IEA.
GO; GO:0003777; F:ATP binding; IEA.
GO; GO:0003777; F:DNA binding; IEA.
PROSITE; PS50067; KINESIN MOTOR DONAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 651 AA; 73091 MW; C4EF79801E603C13 CRC64;
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GO; GO: 0005875; C: interacubule associated cor
GO; GO: 0005824; F: ATP binding; IEA.
GO; GO: 0003677; F: DNA binding; IEA.
GO; GO: 0003774; F: DNA binding; IEA.
InterPro; IPR010996; DNAPOL B. N. like.
InterPro; IPR010996; DNAPOL B. N. like.
InterPro; IPR010752; kinēsin_motor.
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4atches 292; Conservative
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TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 MKRPREEAEATTSSRQRKKSKTDSTESSPNSSMESTGKRKLN----LASLDSAVVERLLK
                                                                                                                                                                                                                                                                                                                       5 RLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDP-PCVRGMDSCSLBIANWRNHQBTLK
                                                                                                                                                                                                                                                                                                                                                                                                                      64 YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRALMDLLQLTR--EEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRILLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKLSQKELLGPPEAKRARGPEEETIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELBAKMLAQKAE-BK
                                                                                                                                                                                                                                                                            Gaps
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                      57.8%; Score 1428; DB 2; Length 6
59.4%; Pred. No. 5.1e-85;
ive 82; Mismatches 106; Indels
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MEDLINE=20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromokinesin required for chromosome alignment
                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                        663 AA; 74538 MW; 3B98B5F3C12C9C22
                                                                    PROSITE; PS00411; KINESIN MOTOR DOMAIN; 1.
PROSITE; PS50067; KINESIN MOTOR_DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
1 1 1
SEQÜENCE 663 AA; 74538 MW; 3B98BSF3C12C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26, Kinesin.
                                                                                                                                                                                                                                             Best Local Similarity 59.43
Matches 287; Conservative
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                                                                                                                                                                                                                      PRALMDLLQLTR--EEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                        242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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                                                                                                                                                                                                                                                                                     LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                         64 YOFDAFYGERSTOODIYAGSVOPILRHLLEGONASVLAYGPTGAGKTHTMLGSPEOPGVI
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog)
Bukaryota, Metacos, Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anvra; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                      8
                                                                                                                                                                      Length 650;
                                                                                                                                                                                       IndelB
                                                                                                                           PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS5067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor Protein.
SEQUENCE 650 AA; 73027 MW; EA8415BC4B9B0F4A CRC64;
                            complex; IEA.
                                                                                                                                                                   57.6%; Score 1423; DB 2;
59.4%; Pred. No. 1e-84;
tive 81; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z
                 GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:intracellular; IEA.
GO; GO:0005874; P:ATP binding; IEA.
GO; GO:0003577; P:DNA binding; IEA.
GO; GO:0003774; P:motor activity; IEA.
InterPro; IPR010996; DNApol_B_Nike.
InterPro; IPR010998; HHH 1.
InterPro; IPR001752; kinesin_motor.
                                                                                       Pfam; PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                              Best Local Similarity 59.48
Matches 287; Conservative
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NCBI_TaxID=8355;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 ARVRVAVRLRPFVDGTAGASDP-PCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 ODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                   Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073177.1; AH73177.1; -
InterPro; IPR010752; Kinesin motor.
InterPro; IPR010994; RuvA_2_like.
PRINTS; PR00325; Kinesin; 1.
PRINTS; PR00325; Kinesin MOTOR DOMAINI; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAINI; 1.
PROSITE; PS00667; KINESIN MOTOR DOMAINI; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 631 AA; 71084 MW; 11E8C9ABBGEBD3F3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                    Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 1422; DB 2;
60.6%; Pred. No. 1.2e-84;
iive 78; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
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Pfam; PF00633; HHH; 1.
Pfam; PF00225; Kinesin; 1.
                           musculus (Mouse).
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                                                                                          NCBI_TaxID=10090;
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Q6L512
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SILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 LKYOFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
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                       371 SRQRKKSKTDSTESSPNSSMESTGKRKIN----LASLDSAVVERLLKLDKILTEKGKKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99425270; PubMed=10493829; Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R., Puhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Coo Y., Xu R.X., Kang H.L., Mitchell S., Eichler B.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q."; BMBL, AC002301; AAC08709.1; -. EMBL, AC002301; AAC08709.1; -.
                                                                                     375 AKRARGPEBEBIGSPEPMAAPASASOKLSPLOKLSSMDPAMLERLLISLDRLLASQGSQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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01-AUG-1998 (TrEMSLrel. 07, Last sequence update)
01-ANG-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin-like DNA binding protein (KID).
Name-A-328A3.2;
Name-A-32BAB-12;
Name-A-32BAB-12;
Manca applens (Hunan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ATP-binding; Microtubule; Motor protein.
SEQUENCE 198 AA; 21567 MW; 1A7FDA95B5A03B37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
PETERPO; F:Motor activity; IEA.
Pfam; PF00225; Kinesin, motor.
SMART; SM00129; KISC; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kinesin motor protein KIF22 (Fragment).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
315
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MEDLINE=97480721; PubMed=9339368;
MEDLINE=97480721; PubMed=9339368;
MIGHITIGLARION, Darkial characterization, and genetic mapping of kinesin-like protein genes in mouse.";
MIGHITICATION, PACA30968.1;
MIGHITICATION, AAC30968.1;
MIGHITICATION, MAC30968.1;
MIGHITICATION, MAC30968.1;
MIGHITICATION, MAC30968.1;
MIGHITICATION, MIGHITICATION, MAC30908.1;
MIGHITICATION, MICHORALIN, IDA.
MICHORALY, MI
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Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.7e-38;
5; Mismatches 6; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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92.6%;
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Best Local Similarity 92.6
Matches 137; Conservative
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Chow T.-Y. Haing Y.-I.C., Chen H.-E., Chen H.-H., Liu S.-M.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chang S.-J., Cheng C.-I., Han S.-Y., Hsiao S.-H.,
Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-P.;
"Oryza sativa BAC OJ1281 H05 genomic sequence.";
Submitted (JUN-2004) to The EMBL/GenBank/DDBJ databases.
EMBL, AC117265; AAT39162.1.
SEQUENCE 584 AA, 64124 MW; EF829C3A15F9190F CRC64;
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                                                                                                                                                                                                                                                                                    6 LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
                                                                                                                                                                                                                                                                                                                     -- YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
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01-JUN-2004 (TrEWBLrel. 27, Last sequence update)
01-JUN-2004 (TrEWBLrel. 27, Last annotation update)
01-JUN-2004 (TrEWBLrel. 27, Last annotation update)
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01-ZUN-2004 (TrEWBLrel. 27, Last annotation update)
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                                                                                                                                                                                    Length 584;
                                                                                                                                                                                 25.6%; Score 633; DB 2; Length 58
36.1%; Pred. No. 5.1e-33;
:ive 89; Mismatches 155; Indels
                                                                                                                                      CRC64;
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                              SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Microtubule; Mctor protein.
SEQUENCE 584 AA; 64124 MW; EF829C3A15F9190F
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        PRINTS; PR00380; KINESINHEAVY
                                                                                                                                                                                          Query Match
Best Local Similarity 36.1
Matches 166; Conservative
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VKLSQK-----BLLGPPEA-KRARGPEEEEIGSPEPMAAP-----ASASQKLSPLOKL 408
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                                                                                                                                                                                REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
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                                                                                                   --YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                              122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                            6 LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
              50;
               Indels
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ilarity 36.1%; Pred. No. 5.1e-33;
Conservative 89; Mismatches 155;
    Local Similarity
                   Matches 166;
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Search completed: November 5, 2004, 18:38:43 Job time : 73.979 secs

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241 NORSSRSHAVLLVKVDORERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINT
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1 MPAAGGSTQQRRREMAAASA......LEAKMLAQKAEEKENHCPTM 512
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/A_CA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-010-033-317-4

US-09-595-684B-35

US-09-724-224-2

US-10-033-317-8

US-09-724-224-2

US-09-724-224-6

US-09-724-224-6

US-09-592-054-6

US-09-723-219-2

US-09-723-219-2

US-09-723-219-2

US-09-723-219-2

US-09-723-219-2

US-09-723-20-8

US-09-724-517-2

US-09-724-517-2

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US-09-150-867-1

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US-09-124-517-4

US-09-124-517-4
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Maximum Match 100%
Listing first 45 summaries
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Sequence 4, Appli
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Sequence 6, Appli
Sequence 29, Appli
        US-09-724-511-2

US-09-723-097-2

US-09-723-097-2

US-09-162-373-1

US-09-467-946-1

US-09-914-259-25

US-09-723-262-6

US-09-723-219-6

US-09-723-219-6

US-09-723-219-6

US-09-723-219-6

US-09-723-219-6

US-09-724-519-6

US-09-724-519-6

US-09-728-156B-2

US-09-728-156B-2

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US-09-728-156B-2
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motor proteins and methods for US-09-724-224-4
US-09-724-224-4
Squence 4, Application US/09724224
Factor No. 6387644
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6387644el motor prot
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT PILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: 09/597,292
FRIOR APPLICATION NUMBER: 09/597,292
NUMBER OF SEQ ID NOS: 8
SQUID NO 4
LENGTH: 512
LENGTH: 512 TYPE: PRT ORGANISM: Human

9 1 MPAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAG Gaps ö 100.0%; Score 2589; DB 3; Length 512; 100.0%; Pred. No. 1.8e-233; cive 0; Mismatches 0; Indels 0 Best Local Similarity 100. Matches 512; Conservative Similarity

360 NFAARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAP 420 SLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSAL

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Query Match
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; Batent No. 6765043
; GENERAL INFORMATION:
; APPLICANT: Bereaud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; RICH REPERSOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.8e-233;
ive 0; Mismatches 0;
                                                                                                                            LEIERLKTKOKELEAKMLAOKAEEKENHCPTM 512
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Best Local Similarity 100.
Matches 512; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 512
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                  RESULT 2
US-10-093-317-4
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WESULT.

US-09-59-684B-35

Sequence 35, Application US/09595684B

Patent No. 6544766

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe
APPLICANT: Bakowicz, Roman

APPLICANT: Valsberg, Eugeni
APPLICANT: Valsberg, Eugeni
APPLICANT: Valsberg, Eugeni
APPLICANT: Wing

TITLE OF INVENTION: Human kinesins and methods of proof
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: Cytop036

CURRENT APPLICATION NUMBER: US/09/595,684B

CURRENT APPLICATION NUMBER: 09/295,612

PRIOR APPLICATION NUMBER: 09/295,612

PRIOR FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 100

SEQ ID NO 35

LENGTH: 65

TYPE: PRT

TYPE: PRT

CORGALISN: Human
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; Sequence 8, Application US/09724224
; Patent No. 6387644
; GENERAL INPORMATION:
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Matches 510; Conservative
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: 00. 6762043e1 motor proteins and methods for
TITLE OP INVENTION: their use
FILE REPERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/093,317
CURRENT FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 09/724,224
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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                 methods for
                                                                                                                                                                                                                               Length 487;
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor proteins and
TITLE OF INVENTION: their use
                                                                                                                                                                                                                             95.3%; Score 2467; DB 3; L
100.0%; Pred. No. 4.4e-222;
tive 0; Mismatches 0;
                                      FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASELSEQ for Windows Version 4.0
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US-10-093-317-8
; Sequence 8, Application US/10093317
; Patent No. 6762043
                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 486; Conservative
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                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
                                                                                                                                                         LENGTH: 487
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US-09-724-224-8
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                                                                                                                               Query Match 95.3%; Score 2467; DB 4; Length 487; Best Local Similarity 100.0%; Pred. No. 4.4e-222; Matches 486; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6387644el motor proteins and methods
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TITLE OF INVENTION: No. 6387644el motor prot
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
TITLE OF INVENTION:
TITLE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
PRIOR PILICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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                        ; TYPE: PRT
; ORGANISM: Human
US-10-093-317-8
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US-09-724-224-2
LENGTH: 487
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TYPE: PRT
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267 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL 326
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302 FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF 361
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                                                                                                                                                                                        Sequence 6, Application US/09724224

Sequence 6, Application US/09724224

Berent No. 6387644

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/09/724,224

CURRENT PILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR APPLICATION NUMBER: 09/597,292

SPRIOR FILING DATE: 2000-06-10

NUMBER OF SEQ ID NOS: 8

SEQ ID NOS: 8

SEQ ID NO 6.
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Patent No. 6762043

GENERAL INFORMATION:

APPLICANT Beraud, Christophe
TITLE OF INVENTION: No. 6762043e1 motor proteins and methods for TITLE OF INVENTION: their use
FILE REPERENCE: 1044

CURRENT FILING DATE: 2002-03-06

PRIOR PILING DATE: 2002-03-06

PRIOR PILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 345; Conservative
                                                                                                      362 AARSKEVIN 370
                                                                 363 AARSKEVIN 371
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; ORGANISM: Human
US-09-724-224-6
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US-10-093-317-6
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US-09-724-224-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF 362
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          AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
                                                                                                                            SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ
                                                                                                                                                                                                                               182 EKVLDILIDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQ
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Patent No. 6762043;
GENERAL INFORMATION:
APPLICANT: Beraud. Christophe
TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use;
FILE REFRENCE: 1044;
CURRENT APPLICATION NUMBER: US/10/093,317;
CURRENT FILING DATE: 2002-03-66;
PRIOR FILING DATE: 2000-11-28;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 369; Conservative
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LENGTH: 370
TYPE: PRT
ORCANISM: Human
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US-10-093-317-2
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                             231 SFRSKLHLVDLAGSERQKKTKAEGDRLKEGININRGLLCLGNVISALGDDKKGSFVPYRD 290
                                                                                                                                                                        349 AELNHLKQ-----QVQQLQVLLLQAHGGTLPGSINAEPSEN---LQSLMEKNQSLVEE 398
                                                                                                                                                                                                                                                                                          444 LLSLDRLLASQGSQGAPLLSTPKRERWVLMKTVEEK-DLEIERLKTKOK-ELEAKMLAOK 501
                                                                                                                                                                                                                                                                                                               LAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPR-- 318
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                                                                             266 QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--VPYRD
                                                                                                                                                 324 SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFINESLQPHA
                                                                                                                                                                                                                      384 IGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09592054
Patent No. 6440684
GENERAL INFORMATION. Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: their use
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CURRENT PELLING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
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Best Local Similarity
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ORGANISM: Human
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                                                                                                                                                                                                                                                                        VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 206
                                                                                                                                                                                                                                                                                                                                            LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 266
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                                                                                                                                                                                                    GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                27 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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Patent No. 6440684

GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Renneth
ITILE OF INVENTION: No. 6440684el motor proteins and methods for
ITILE OF INVENTION: their use
FILE REFERENCE: 1016
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                               0; Indels
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                                                                                                            DB 4;
                                                                                                          68.1%; Score 1763; DB 4;
100.0%; Pred. No. 2e-156;
ive 0; Mismatches 0
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                                                                                                                           Best Local Similarity 100.
Matches 345, Conservative
SEQ ID NO 6
LENGTH: 346
TYPE: PRT
ORGANISM: Human
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ORGANISM: Human
                                                            ; OKGANISM: AU
US-10-093-317-6
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                                                                                                          Query Match
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Sequence 2, Application US/09592054 Patent No. 6440684 GENERAL INFORMATION:
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; Sequence 2, Application US/09572191
; Patent No. 6355466
; GENERAL INFORMATION:
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466 DLQKLVETLEDQE 478
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DLQKLVETLEDQE 458
 494 EAKMLAQKAEEKE 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 32.0
Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Human
US-09-592-054-2
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 1232
                                                                                                 US-09-592-054-2
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284 VPYRDSKLTRLLQDSLGGNSHTLMIACVSPADSNLEETLNTLRYADRARKIKNKPIVNID 343
                              379 LOPHALGPVK--LSQKELLGPPEAKRARGPEEERIGSPEPMAAPASASQKLSP-LOKLSS 435
                                                     --TLPGSITVEPSENLQSLME 388
                                                                                            436 MDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-EL 493
                                                                                                                    90 OFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQ 144
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APPLICANT: Einer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.0%; Score 568.5; DB 4; Length 522; 32.3%; Pred. No. 2.3e-44; ive 97; Mismatches 162; Indels 75
                                                             344 POTABLNHLKOOVQOLOVL----LLOAHGG----
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Patent No. 6440684
GENERAL INFORMATION:
                                                                                                                                                               494 EAKMLAQKAEEKE 506
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Best Local Similarity 32.3
Matches 159; Conservative
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US-09-592-054-4
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261 LAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR-- 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY
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APPLICANT: Beraud, Christophe
APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for ITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REPERENCE: 1016
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                            TYPE: PRT
ORGANISM: Human
                                     SEQ ID NO 2
LENGTH: 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 VRVAVRLRPFVD--GTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTWLGSPEQP-----GVIPRA---L 152
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                                                                                            methods for
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APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6379912e1 motor proteins and methods for
FILE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/723,262
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/572,191
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
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APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6355466el motor proteins and
TITLE OF INVENTION: their use
TITLE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/572,191
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.7%; Score 561; DB 3; 30.9%; Pred. No. 5.4e-43;
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Patent No. 6379912
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ORGANISM: Human
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                                         ; Score 561; DB 3; Length 13
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97; Mismatches 192; Indels
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Job time : 22.0023 secs
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ilarity 30.9%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5, 2004, 18:34:12; Search time 105.087 Seconds (without alignments) 1747.786 Million cell updates/sec US-10-797-893-4

2589 1 MPAAGGSTQQRRREWAAASA.....LEAKWLAQKAEEKENHCPTM score: Sequence: Title: Perfect (

512

2002273 seqs, 358729299 residues Searched:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing, first 45 summaries

geneseqp20018:* geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Adc23340 Human kin	Adq60230 Human mic	Adq09240 Human KNS	Adc23344 Human kin	Adq60234 Human mic	Adk40973 Novel hum	Aab56650 Human pro		Adq60228 Human mic	Adc23342 Human kin	Adg60232 Human mic	Abb71112 Drosophil	Abb65183 Drosophil	Adk40926 Novel hum	Add49938 Human lun	Add18924 Human dis	Adj70347 Human hea	Adk40901 Novel hum	Abg70993 Human HsK	Abg70992 Human tar	-	Abu53123 Intracell	Aau76957 Novel hum	Adc31082 Human nov	Adil5915 Human PP
	QI		ADC23340	ADQ60230	ADQ09240	ADC23344	ADQ60234	ADK40973	AAB56650	ADC23338	ADQ60228	ADC23342	ADQ60232	ABB71112	ABB65183	ADK40926	ADD49938	ADD18924	ADJ70347	ADK40901	ABG70993	ABG70992	ABG70991	ABU53123	AAU76957	ADC31082	ADI15915
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	Score		2589	2589	2577	2467	2467	2419	2151	. 1873	1873	1763	1763	616	593	578.5	574.5	574.5	574.5	574.5	573.5	568.5	568.5	268	568	568	268
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26 27 28	300	3 7 F	34 35	36 37	8 6 8 7 8 8	4 4 1	42	4 4 4 5

ALIGNMENTS

RESULT 1

human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. Human kinesin-like DNA binding protein (KID) (SeqID 4). /note= "Encoded by CA" Location/Qualifiers Š ADC23340 standard; protein; 512 28-NOV-2000; 2000US-00724224. (first entry) Key Misc-difference 2 Homo sapiens US6387644-B1 18-DEC-2003 14-MAY-2002. ADC23340; ADC23340

20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. (CYTO-) CYTOKINETICS INC.

WPI; 2003-706919/67. Beraud C;

N-PSDB; ADC23339

Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.

Claim 1; SEQ ID NO 4; 26pp; English.

This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor

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domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplaais, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 4) of the invention.
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Sequence 512 AA;

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                                             MPAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAG
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Human microtubule motor protein #2.
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        ADQ60230 standard; protein;
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                           23-SEP-2004
                 ADQ60230;
RESULT 2
ADQ60230
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Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.

US6762043-B1 13-JUL-2004

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or concerning to a carget protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating callular consideration disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders and inflammatory bowell disease and consideration induced after medical procedures including surgery and candidate and procedures including surgery and candidate and procedures including surgery and candidate hy the mucleic acid featured as SBQ ID NO:3, but this does not NQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINT 300 SLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSAL 360 361 NFAARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAP 420 New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and 181 YQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRL 61 ASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQ 61 ASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQ 121 NASVLAYGPIGAGKTHIMLGSPBQPGVIPRALMDLLQLIREEGAEGRPWALSVIMSYLEI 1 MPAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAG 121 NASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEI Gaps ö Length 512; Indels 100.0%; Score 2589; DB 8; 100.0%; Pred. No. 5.2e-233; ive 0; Mismatches 0; Claim 1; SEQ ID NO 4; 26pp; English. 20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. 28-NOV-2000; 2000US-00724224. 06-MAR-2002; 2002US-00093317 Local Similarity 100. Les 512; Conservative (CYTO-) CYTOKINETICS INC. WPI; 2004-532491/51 Sequence 512 AA; inflammation 241 301 301 Query Match Beraud Matches d g ò 셤 ò g 8 셤 ò ò

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The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive to a THAP/Chemokine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a cell comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family comprising a transcription between a nucleic acid and a THAP-family collypeptide or its biological fragment, or a nucleic acid and a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-family polypeptide or its biological combinant THAP-family polypeptide or its biological symptoms associated with a condition mediated by a THAP/chemokine complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                        thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
ASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKD
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                                                                                                                                                                                                                                                                                 ADQ09240 standard, protein; 665 AA
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ta a THAP responsive element or that modulates transcription

at a THAP responsive element or that modulates the transport of a

CC demokine into the nucleus; (10) methods for reducing the symptoms

associated with a condition selected from excessive or insufficient

angiogenesis, inflammation, metastasis of a cancerous tissue, excessive

CC insufficient apoptosis, cardiovascular disease and neurodegenerative

diseases; symptoms associated with a condition resulting from the

activity of a chemokine or a THAP-family polypeptide in an individual; or

comprising a THAP-family polypeptide in an individual; (11) a vector

comprising a THAP-family polypeptide in an individual; (11) a vector

comprising a THAP-family polypeptide or nucleic acid

comprising a detectable product; (12) a genetically engineered cell

comprising the vector described above or that expresses a THAP-family

comprising the vector described above or that expresses a THAP-family

comprising a nucleic acid comprising a THAP responsive promoter,

comprising the vector described above or that expresses a THAP-family

comprising an nucleic acid comprising a THAP responsive promoter,

craction has antiangiogenic, antinflammatory, cardiovascular,

craction has antiangiogenic, antinflammatory, cardiovascular,

cromposition has antiangiogenic, antinflammatory, cardiovascular,

cytostatic, neuroprotective and osteopathic activities, and can be used

composition has mainangiogenic ariand series or insufficient

composition has present of a THAP responsive gene. Modulation us useful

composition has present sequence is cancerous tissue, excessive

con insufficient apoptosis, cardiovascular disease or neurodegenerative

con insufficient apoptosis, cardiovascular disease or neurodegenerative

confidence or invarior. 181 122 121 242 241 301 422 421 61 2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS 123 SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ EKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQ RSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF 63 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA **EKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQ** RSSRSHAVILVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF 3 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS **AARSKEVINRPFINESLOPHALGPVKLSQKELLGPPEAKRARGPEEEIGSPEPMAAPAS AARSKEVINRPFTNESLOPHALGPVKLSOKELLGPPEAKRARGPEEEIGSPEPMAAPAS** Gapa ö 0; Indels Pred. No. 1.1e-231; 0; Mismatches 0: T-99.5%; Score 2577; 99.55, 100.0%; Pre-Matches 510; Conservative Query Match Best Local Similarity Sequence 665 AA; 183 62 122 182 243 242 303 302 363 362 888888888888888888888888888888888 a 셤 ò ઠે 셤 ð d ઠ 셤 ò 셤 ò 셤

LESULT 4 DDC23344 D ADC23344 standard; protein; 487

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422 ASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKOLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This, polypeptide sequence is human KID protein (SeqID 8) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                           human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a candidate agent as modulator of function of a targ
protein for treating cellular proliferation disorders by adding
candidate agent to a mixture of the target protein that
directly/indirectly produces ADP or phosphate.
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                                                                                Human kinesin-like DNA binding protein (KID) (SeqID 8)
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100.0%; Pred. No. 1.3e-221;
ive 0; Mismatches 0;
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20-JUN-2000; 2000US-00597292.
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                                                 (first entry)
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                 ADC23344;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasts, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                                                                                                                                                                                          422 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEARMLAQKAEEKE
242 REGKLYLIDLAGSEDNRRTGNKGLRLKESCAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                        TRILODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLOPHALGP
                                                                             302 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                                                                       387 VKLSQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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              proliferation disorders such as cancer, hyperplasias, restencies, cardiac Appertophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and sucoliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention.
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 screening for modulators of motor proteins useful for treating cellular
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                                                                                                                                                                                 / Match 95.3%; Score 2467; DB 8; Length 487; Local Similarity 100.0%; Pred. No. 1.3e-221; Nes 486; Conservative 0; Mismatches 0; Indels (
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (b); (c) hybridizes under stringent conditions to (a) and complement of complement of complement of a catalytic domain, a C. terminal domain, a coiled-coil structure region, a spacer region and a C. terminal domain, a coiled-coil structure region, a spacer region and a C. terminal domain, a coiled-coil structure region, a spacer region and a C. terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers. C. terminal-associated diseases or disorders, cardiovascular disease, brain or cultural associated diseases, and metabolic disorders. The disorders are control or peripheral nervous system, Alzheimer's disease, to preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, corrections, infections caused by fungi, ocular diseases, migraines, pain, bacteria, infections caused by fungi, ocular diseases, migraines, pain, centeria, infections caused by fungi, ocular diseases, migraines, pain, diseasus, metabolic disorders and organ transplant correction. This sequence corresponds to one of the kinase polypeptides of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA
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Pred. No. 4.1e-217;
0; Mismatches 0;
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100.0%; Pre
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                                                                                                                                                       31-DEC-2001; 2001US-0343169P
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                                                                                                                                                                                                                                                         Grigoriev IV, Sudarsanam
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Best Local Similarity 100.
Matches 479; Conservative
                                                                                                                                                                                               (GRIG/) GRIGORIEV I V
(SUDA/) SUDARSANAM S.
                                                                                                                                                                                                                                                                                                                                                                                                disorders.
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                                     WO2003057841-A2
Homo sapiens.
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AAB56650;

AAB56650 RESULT

Human

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human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                               302 KLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFARSKEVINRPFTNESLQPHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQ
                                                                     2 GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHO
                                                                                                            ETLKYQPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ
                                                                                                                                                                                                                                                                                                                                 RQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDS
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                                                                                                                                                                                   PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG
                                                                                                                                                                                                                                                           NILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human kinesin-like DNA binding protein (KID) (SeqID 2).
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC23338 standard; protein; 370 AA
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20-JUN-2000; 2000US-00597292.
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   424; Conservative
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                          369
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                                                                                                                429
                                                                                                                                                      481
                                                                                                                                                                                         488
                             FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF
                                                                             AARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPAS
                                                                                                                                                                          ASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERWVLMKTVEEKDL
                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer antigen protein sequence SEQ ID NO:1228.
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                                                                                                                                                                                                                                                                                        AAB56650 standard; protein; 460 AA
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ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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(HUMA-) F (ROSE/) F

Identifying a candidate agent as modulator of function of a target

N-PSDB; ADC23337

Score 2151; DB 3; Length 460; Pred. No. 4.6e-192;

83.1%; 95.9%;

Query Match Best Local Similarity

Sequence 460 AA;

isolated microtubule motor protein, useful for screening modulators

WPI; 2004-532491/51

New

Beraud C;

99US-00295612.

20-APR-1999; 20-JUN-2000;

28-NOV-2000; 2000US-00724224 (CYTO-) CYTOKINETICS INC

06-MAR-2002; 2002US-00093317

13-JUL-2004

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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP to phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomedulators and antinfilammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 2) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
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protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                Length 370;
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                                                                                                                                                                                                                                                                                                                                                                               72.3%; Score 1873; DB 7; L
100.0%; Pred. No. 3.5e-166;
iive 0; Mismatches 0;
                                                                   Claim 1; SEQ ID NO 2; 26pp; English.
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Matches 369; Conservative
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                                                                                                                                                                                                                                                                                                                                              Sequence 370 AA;
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The invention traces to numeral mistocubuse muctor processing and the invention traces to numeral mistocubuse muctor processing acidis encoding them. The invention which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind ca target proteins, methods to identify candidate agents that bind ca target protein or act as a modulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cardiac hypertrophy, immune disorders and inflammation, for treating associated with KID and for inhibiting KID and for treating autoimmune associated with KID and for inhibiting KID and for treating autoimmune cassociated with KID and for inhibiting KID and for treating autoimmune cassociated with KID and for inhibiting KID and for treating autoimmune considers associated with KID and for inhibiting KID.

Consideration induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to human microtubule motor proteins and the nucleic
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                                                                                                                                                                                                                                                                                                                      for treating cellular proliferation disorders such as senening modulat hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2; 26pp; English
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Matches 369; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 370 AA;
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147 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLBIYQEKVLDLLDPASGDLVIREDCRGNI

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using method or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, therapy, they can be used for the treatment of cancer, hyperplasise, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 6) of the invention.
                                                                                                                                                                                                                                               human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 346;
                                                                                                                                                                                                                      Human kinesin-like DNA binding protein (KID) (SeqID 6).
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68.1%; Score 1763; DB 7; L
Best Local Similarity 100.0%; Pred. No. 6.4e-156;
Matches 345; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 6; 26pp; English
                                                                                                                    ADC23342 standard; protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2000; 2000US-00724224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTO-) CYTOKINETICS INC
                           362 AARSKEVIN 370
363 AARSKEVIN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-706919/67.
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                         18-DEC-2003
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                                                                                                                                                        ADC23342;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, protein or act as a modulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular screening for modulators of motor proteins useful for treating disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders
                                                    266
                                                                                                                           REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 326
              181
                                                                                                                                                     242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                        TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 371
                                                                                                                                                                                                                               Claim 1; SEQ ID NO 6; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microtubule motor protein #3.
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; ADQ60231.
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GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 86

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associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention.
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                                                                                                                                                                                                               GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                       GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
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                                                                                                                                                                                                                                                 VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 40128; 21pp + Sequence Listing; English
                                                                                                   Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                TRILIQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                   TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 371
                                                                                                                         0; Indels
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                                                                                                68.1%; Score 1763; DB 8; L
100.0%; Pred. No. 6.4e-156;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB71112 standard; protein; 784
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                      Matches 345; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
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                                                                                                             Similarity
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                                                                         Sequence 346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
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                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    RE--RGSGVYVPNLHAINCKSVEDMIKVMQVGNKNRTVGFTNMNEHSSRSHAIFMIKIEM 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463
          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eluciary for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176, and the encoded proteins (ABB57737-sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                               83 HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD-TETNTIKVGKLNLIDLAGSERQSKTGASAERLKEASKINLALSSLGNVISALAESSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 HVPYRDSKLTRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYASRAKSIQNQPIKNE
                                                                                                                                                                                                                                                                                                                    GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 REDCRGN-ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 RERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 DPQ-----DAKLKEYQEEIERLKRLIGPQQQRSEKQVTAKKQRVKKPKKETVTKEMSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQG
                                                                                                                                                                                                                                                                                             37 TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLQPHALGPVKLSQ-----KELLGPPEAKRA------RGPEEEI-----
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                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APLLSTPKRERMVLMKTVEEKDLEIER-----LKTKQKELEAKMLAQKAEE
                                                                                                                                                                                                                               Length 784;
                                                                                                                                                                                                                             Score 616; DB 4; Length 79
Pred. No. 6.1e-48;
1; Mismatches 183; Indele
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                                                                                                                                                                                                                               23.8%;
33.1%;
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                                                                                                                                                                                                                          Query Match 23.8*
Best Local Similarity 33.1*
Matches 176; Conservative
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                                                                                                                                                                                              Sequence 784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical
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   23-MAR-2001; 2001WO-US009231
            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Best Local Similarity 33.99
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                ----LAQKAEEKE
                                   Adams M,
                                            WPI; 2001-656860/75.
                         (PEKE ) PE CORP NY
                                                N-PSDB; ABL09286
                                                                                                                                      Sequence 677 AA;
                                   Venter JC,
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antiparkinsonian; virucide, antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; neurological disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
                                                                                                                                                                          cytostatic; immunomodulator; cardiant; neuroprotective; nootropic;
                                ADK40926 standard; protein; 1237
                                                                                                                                        Novel human kinase protein #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-DEC-2001; 2001US-0343169P.
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                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003057841-A2.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                      06-MAY-2004
                                                                    ADK40926;
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RESULT 14
                 ADK40926
                                                                  497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIDLAGSEDNRRTGNKGIRLKESGAINTSLFVLGKVVDALNQG-LPRVPYRDSKLTRLLQ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNE----SLQPHALGPV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB12072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 KLSQKEL-LGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 ARLRKOLEEGDSLEEEPPSSEEEEDTADDELEAPLEIELESSTIQAVEKKPKKKREK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 LDRLLASQGSQGAPLLSTPXRERMVLMKTVEEKDLEIERLKTKQKELEAKM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP---GVIPRALMDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 22341; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.9%; Score 593; DB 4; Length 677; 33.9%; Pred. No. 6.9e-46; Live 78; Mismatches 190; Indels
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474 GGENLLEKAQTQE 486
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The invention elates to novel isolated, enriched or purified nucleic acid molecule molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprise an acquence that: (a) encodes a naturally occurring kinase polypeptide; (b) is a complement of (a), (c) hybridizes under stringent conditions to (a) and coordess a naturally occurring kinase polypeptide; (d) encodes the coordespoint of an encodes an actually occurring kinase polypeptide; (d) encodes the coordespoint of an except that it lacks one or more, but not all, of an opportune of the canalytic domain, a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are perferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, brain, viral infections infections caused by fungi, ocular diseases, migraines, pain, cacteria, infections mood disorders, appropriate original disorders, dyskinesias, metabolic disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant criedian in this sequence corresponds to one of the kinase polypeptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
New isolated, enriched or purified nucleic acid molecule encoding a
kinase polypeptide, useful for treating cancer, immune-related diseases,
cardiovascular disease, brain or neuronal-associated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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22.3%; Score 578.5; DB 7;
Best Local Similarity 32.4%; Pred. No. 4.1e-44;
Matches 157; Conservative 97; Mismatches 172;
                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 33; 491pp; English.
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265
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                                                                                                                                                                                                                  384 IGPVKLSQKELIGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLER 443
                                                                                                                                                                                                                                                         444 LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-ELEAKMLAQK 501
 ----VRGMDSCSLEIANWRNHQETLKYQFDAF 94
                                                                                                                                   YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQP--GV
                                                  : | :::: : | |::: : | ||:||||| ||:|||::| |:
FDPCTEQEBVENKAVAPLIKGIFKGYNATVLAYGQTGSGKTYSMGGAYTAEQENEPTVGI
                                                                              IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIREDCRGN
                                                                                          ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR
                                                                                                                                                             QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--VPYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, lung cancer antigen, cytostatic, lung cancer, gene therapy,
vaccine, T-cell; tumour.
                  VRVALRCRPLVPKEISEGCOMCLSFVPGETQVVVGTDK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lung specific tumour antigen L 1447p.
                                                                                                                                                                                                                                                                                                                                                                                                   ADD49938 standard; protein; 1232 AA.
VRVAVRLRPFVDGTAGASDPPC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bangur CS, Switzer A;
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05-OCT-2001;
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The invention relates to an isolated polynucleotide (a) comprising any of the 666 fully defined nucleotide sequences appearing as ADD499269 - CADD49935, ADD49936, and ADD49938, complements of (a); sequences of a teast 20 contiguous residuaes of (a); sequences that hybridise to (a) under highly stringent conditions; sequences having at least 75 or 90% identity to (a); or degenerate variants of (a). Also included are an isolated polypeptide (b) (comprising; sequences encoded by the new polynucleotide; any of the 4 amino acid sequences fully defined in the specification; or sequences having at least 70 or 98% identity to the sequence in (a) or (b)), an expression vector control sequence, a host colynucleotide operably linked to an expression control sequence, a host coll transformed or transfected with the above expression vector; an isolated antibody, or its antigen-binding fragment, that specifically binds to the above polypeptide, an oligonucleotide that hybridises to the converse entities of the finds to mean of the conditions, a finite mean of the conditions. fusion protein comprising at least one polypeptide cited above, detecting the presence of a cancer in a patient (comprising obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide, or with the oligonucleotide cited above; detecting in the sample an amount of the polypeptide that binds to the binding agent, or an amount of a polypurcleotide that hybridises to the oligonucleotide; and comparing the amount of polypeptide, or polypurcleotide that hybridises to the oligonucleotide, to a predetermined cut-off value and then determining the presence of a cancer in the patient), a method for stimulating and/or expanding T-cells specific for a tumour protein (comprising contacting T-cells with the above 225 144 200 DCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRER 260 polypeptide, polynuclectide or antigen-presenting cells that express the polynuclectide, under conditions and for a time sufficient to permit the stimulation and/or expansion of Teells), an isolated T-cell population comprising T-cells prepared by the method, a composition comprising a first component selected from physiological carriers and immunostimulants and a second component selected from the above polypeptide, polynuclectide, antibody, fusion protein, T-cell population and antigen-presenting cells that express the above polypeptide, and antigen-presenting cells that express the above polypeptide, cesponse in a patient (comprising administering to the patient the above composition) treating lung cancer in a patient (comprising administering to the patient the above composition and a diagnostic kit (comprising: at least one oligonucleotide cited above; or at least one antibody cited above and a detection reagent comprises a reporter group). The composition and detection reagent comprises a reporter group). The composition and 83 49 QPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQ 145 P--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIRE DPKEGIKIVGLTEKTVLVALDTVSCLEQGNNSRTVASTAMNSQSSRSHAIFTISLEQRKK 45 VRVAVRLRP-------FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY VRVALRCRPLVPKEISEGCOMCLSFVPG----EPQVVVGTDK-----SF LAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--Gaps methods are useful in diagnosing, preventing and treating cancer, particularly lung cancer. The present sequence is a lung cancer-associated antigen of the invention. 75; ; Score 574.5; DB 7; Length 1232; Pred. No. 9.7e-44; 97; Mismatches 161; Indels 75; 22.2%; Conservative Best Local Similarity Matches 160; Conserv Sequence 1232 AA; 10 9 20 201 166 261 Query Match 용 ð 셤 ò 유 8 셤 δ ઠે

VPYRDSKLTRILQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNES 378

SDKNSSFRSKLHLVDLAGSEROKKTKAEGDRLKEGININRGLLCLGNVISALGDDKKGGF

226

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New isolated polypeptides and polynucleotides useful for diagnosing, preventing and treating cancer,

WPI; 2003-844452/78. N-PSDB; ADD49936.

Claim 1; SEQ ID NO 670; 250pp; English

Search completed: November 5, 2004, 18:44:39 Job time : 107.087 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model - protein search, using OM protein 5, 2004, 18:34:12; Search time 10.7872 Seconds (without alignments) 3300.235 Million cell updates/sec November Run on:

US-10-797-893-2 1878 Title: Perfect score:

1 MAAGGSTQQRRREMAAASAA......FYLDTVSALNFAARSKEVIN 370 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq Maximum DB seq

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

	Description	kinesin-like DNA b	kinesin-like prote	kinesin-related pr	F25116.11 protein	kinesin heavy chai	kinesin-related pr	probable kinesin-1	kinesin-like prote	F22M8.8 protein -		kinesin homolog F2	probable kinesin-r	kinesin-related pr	probable kinesin-1	kinesin-related pr	kinesin-related pr	Q		kinesin-related pr	chromokinesin - ch	kinesin-related pr	c	kinesin homolog KH	kinesin-related pr	kinesin-like prote	microtubule-associ	kinesin heavy chai	kinesin-like prote	kinesin-like prote
SUMMARIES	OI	862328	T48258	A55236	A86319	T18277	T47525	T40594	151617	D86151	T30335	T06733	H84777	T02017	B84687	S38982	A48669	A56921	B44259	S64238	A56514	A57107	E84792	A53939	T14156	T48959	A54803	T10164	B48835	24
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de	Query	88.7	31.7	29.6	29.3	29.1	28.6	28.2	28.3	28.3	28.1	28.0	27.9	27.8	27.6	27.4	27.4	27.4	27.3	27.3	27.3	27.3	27.2	27.1	27.1	27.1	27.0	27.0	56.9	26.8
	Score	1665	594.5	555.5	550	547	536.5	536	532	531.5	527.5	525	524	521.5	517.5	514.5	514	514	513.5	513.5	513.5	513	511.5	509.5	509.5	508	507.5	507	504.5	504
	Result No.		7	n	4	ß	9	. 7	œ	o	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	25	56	27	28	59

YQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRL 239

121 AKVVLAYGPTGAGKT-THAGOPRATWGDPAGSHGPPAAHKGGGCRGPAMGLSVTMSYLEI

NORSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINT 299

240

180

240 NQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINT

SLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSAL 359

NFAARSKEVIN 370 360 NFAARSKEVIN 370

300 360

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179

SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQN 120 SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGGN 120 AS-VLAYGPIGACKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEI 179

19 61 121

1 MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA

1 MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA

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kinesin-like spind	kinesin-like prote	kinesin [imported]	hypothetical prote	kinesin [imported]	kinesin-like prote	kinesin heavy chai	kinesin-related or	kinesin-like prote	kinesin-like heavy	kinesin-related or	kinesin heavy chai	kinesin-like prote	kinesin-related pr	kinesin-like prote	kinesin heavy chai
G02157	A55289	T51930	T20621	T51932	T40128	A41919	S58691	T38378	T51360	JC5831	S44868	C48835	JN0114	T15822	837711
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26.7	26.6	26.5	26.4	26.4	26.3	26.1	26.1	26.0	26.0	25.9	25.9	25.7	25.7	25.7	25.7
01	200	498.5	495.5	495	494.5	491	490	488.5	488	485.5	485.5	483	482.5	482.5	482
S															

ALIGNMENTS

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Cibate: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
Cibate: 23-Aug-1996 #sequence_revision 15-Marithmary 1996
A;Title: Kid, a novel Kinesin-like DNA binding protein, is localized to chromosomes and A;Reference number: S62328; MulD:96174806; PMID:859929
A;Accession: S62328
A;Accession: S62328
A;Accession: S62328
A;Accession: S62328
A;Accession: S62328
C;Cypatefaminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-65 -TOK>
C;Cypatefamily; kinesin motor domain homology
C;Keywords: ATP; nucleotide binding; P-loop
F;128-135/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.7%; Score 1665; DB 2; Length 6 91.4%; Pred. No. 2.4e-125; ive 1; Mismatches 29; Indels
kinesin-like DNA binding protein KID - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.4<sup>‡</sup>
Matches 339; Conservative
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10;

31;

Indels

Length 784;

138

9

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RiTheologis, A.; Beker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, I. A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cross-references: UNIPROT: Q9FZ77; GB: AE005172; NID: 99795601; PIDN: AAF98419.1; GSPDB: GN(
                       A;Cross-references: FlyBase:rbgIuvousce.
C;Function:
C;Function:
M;Description: may be part of a motor protein that provides anterograde fast axonal trans.
A;Description: may be part of a motor protein KIF3; kinesin motor domain homology
C;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C;Reywords: ATP; coiled coil; microtubule binding; mucleotide binding; P-loop
F;1249/Domain: head globular #status predicted <HGL>
F;20-350/Domain: kinesin motor domain homology <KMOT>
F;106-113/Region: nucleotide-binding motif A (P-loop)
F;350-880/Domain: helical rod #status predicted <HGL>
F;511-784/Domain: tail globular #status predicted
F;511-784/Domain: tail globular #status predicted
F;112/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GNDELMGIIPRIFEQIWLHINRTEN-----PQPLVDVSYLEIYMEELRDLLKPNSKHLEV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 RERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F25116.11 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 ARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK-----YQFDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 REDCRGN-ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN
                                                                                                                                                                                                                                                                                                                                                                                                                                               HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 RVPYRDSKLTRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 HVPYRDSKITRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYGSRAKSIQN 346
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38.6%; Pred. No. 5.6e-36;
ive 62; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                   Query Match 29.6%; Score 555.5; DB 1;
Best Local Similarity 39.5%; Pred. No. 2.4e-36;
Matches 140; Conservative 56; Mismatches 127;
                  Cross-references: FlyBase:FBgn0004381
Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
A, Gene: FlyBase:Klp68D; KLP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: A86319
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Best Local
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Kinesin-related protein KLP68D - fruit fly (Drosophila melanogaster)

N;Alternate names: Kinesin-like protein 5; KLP5

C;Species: Drosophila melanogaster

C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004

C;Accession: A5236; B41298

R;Pesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.

C.ell Biol. 127, 1041-1048, 1994

A;Title: Characterization of the KLP68D kinesin-like protein in Drosophila: possible roll

A;Reference number: A55236

A;Accession: A55236

A;Molecule type: mRNA

A;References: UNIPROT:P46867; GB:U15974; NID:G595912; PIDN:AAA69929.1; PID:G565096

A;Accession: A5404. Sci. U.S.A. 88, 8470.8474, 1991

Proc. Natl. Acad. Sci. U.S.A. 88, 8470.8474, 1991

A;Reference number: A41298; MUD:92020874; PMID:1924306

A;Accession: A12286; MUD:92020874; PMID:1924306

A;Accession: A12298; MUD:92020874; PMID:1924306

A;Accession: A12298; MUD:92020874; PMID:1924306
                                    STILSMCEKTRSRAE-----ISYYEVYMDRCWDLLEVKDNEIAVWDDKDGQVHLKGLS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYG-ERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRAL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Nap position: 5
A;Introns: 58/3; 128/2; 184/3; 310/1; 378/3; 480/2; 501/3; 535/1; 607/3; 628/3
A;Note: T1E22.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 ARVRVAVRLRPFV-----DGTAGASDPPCVRGMDSCSLEIANWRNHQETLK---YQFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 MDLLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Residues: 'TC',222-337,'VRGQV' <STE>
A;Cross-references: GB:M74431; NID:g157791; PIDN:AAA28658.1; PID:g157792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 664;
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A;Experimental source: cultivar Columbia; BAC clone T1E22
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38.6%;
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Best Local Similarity 38.6
Matches 131; Conservative
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Cyaccession: T47253
RiJordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, Submitted to the Protein Sequence Database, March 2000
A;Reference number: 224468
A;Reference number: 224468
A;Reference number: 224468
A;Residuus: preliminary
A;Molecule type: DNA
A;Residues: 1-1058 cJCR>
A;Experimental source: cultivar Columbia; BAC clone F16L2
        20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 134; Conservative
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Best Local Similarity
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A; Residues: 1-784 < PUR>
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C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Accession: T18377
R;deHostos, E.L.; McCaffrey, G.; Vale, R.D.
R;deHostos, E.L.; McCaffrey, G.; Vale, R.D.
A;Reference number: Z18853
A;Accession: T18277
A;Accession: T18277
A;Accession: T18277
A;Accession: T18277
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1254 vDEH>
A;Coss-references: UNIPROT:Q94463; EMBL:U41289; NID:g1526990; PID:g1526991; PIDN:AAB077
                                                                                                                                                                                                      213
                                                                                                                                                                                                                                150 SRILVFURLRPMGKKERENGSRCCVKVI.NKRDVYLTEFTWENDYLRLKRLRVRHFTFDSS 209
                                                                                                                                                                                                                                                                                                                                            214 PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR--QREGKLY 271
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                                                                                                                    210 FPETTTQQEVYSTTTGDLVEAVLEGRNGSVFCYGATGAGKTYTWLGTMENPGVMVLAIKD
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kinesin-related protein-like - Arabidopsis thaliana N;Alternate names: protein F16L2.60 C;Species: Arabidopsis thaliana (mouse-ear cress)

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A;Map position: 3
A;Introms 56/2; 99/3; 151/3; 310/3; 343/2; 395/3; 419/1; 444/3; 462/3; 489/3; 527/1; 55
A;Note: F16L2.60
C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology
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A;Experimental source: strain 972h-; cosmid c649
F;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, July 1998
A;Reference number: 221861
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A;Cross-references: EMBL:AL031154; PIDN:CAA20063.1; GSPDB:GN00067; SPDB:SPBC1685.15c
A;Experimental source: strain 972h-; cosmid c1685
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V.; Rajandream, M.A.; Barrell, B.G.
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                                                                                                                                                                                                                                                                                                                              3 SIQQRRGGIVSLSPAQTPRSSDKSARESRSSESNSTNRNDKEKGVNVQVILRCRPLSEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable kinesin-like protein - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS------PEQPGVIPRALMDLLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 STQQRRREMAAASAA----AISGAGRCRLSKIGATRRPPPAR---VRVAVRLRPFVDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                        55;
                                                                                                                                                          Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRLLRESLGGKTKTCVIATISPSIHCLEETLSTLDYAHRAKNIKN 392
                                                                                                                                                                                                                            Indels
                                                                                                                                                          28.6%; Score 536.5; DB 2; 33.1%; Pred. No. 1.2e-34; ive 77; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREEGAEGRPWALSVTMSYLEIYQEKVLDLLDP----
                                                                                                                                                                                                                                                                                                                                                                                                                58 AGASDPPCVRGMDSCSLEIANWRNHQETLKYQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Date: 03-Dec-1999 #sequence_revision 03-Dec
C;Accession: T40594, T39531
R;Purnelle, B.; Goffeau, A.; Lyne, M.; Wood,
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21939
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Rithelogis, A.; Beker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R; Theologis, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

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Nature 408, 186-820, 2000

Natures, Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.L.; J.J., J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rizoney, T.; Rouney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II A; Muthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II A; Muthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, II A; Meference number: A86141; MuID:21016719; PMID:11130712

A; Retern commer: A86141; MuID:21016719; PMID:11130712

A; Molecule type: DNA

A; Mesidues: 1-885 - STO>
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                                                                            152 MDLLQLTREEGAEGRP-WALSVTMSYLEIYQEKVLDLLDPA---SGDLVIREDCRGNILI 207
                                                                                                                                                                                   PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQRE 267
                                                                                                                                                                                                     GKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR---VPYRDSK 324
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                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRTVGATRINORSSRSHAVLLVKV------DORERLAPFRQ-----REGKLYL
                                                                                                                                                                                                                                                                                                                                                                                                                        P. 2206.8 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 GASDPPCVR---GMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEGONASVLAYGPTGACKTHTM--LGSPEQP--GVIPRALMDLLQLTREEGAEGRPWALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::|||::|| | | ||||| | ::: | || || ||:::|| : :|
187 ISVSYLQLYMETIQDLLDPTNDNIAIVEDPRTGBVSLPGATHVEIRNQQNFLELLQLGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAAGGSTQORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRP--FVDGTA
VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETL----KYQFDAFYGERS
                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 885;
                                                                                                                                                                                                                                                                                                                               LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
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                                                               99 TOODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
28.3%; Score 531.5; DB 2;
Best Local Similarity 34.4%; Pred. No. 2.4e-34;
Matches 137; Conservative 72; Mismatches 150;
                                  VRVÁLRCRPLVP-----
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                                                                                                                                                                                              119
                                                                                                                                                                                                              NASVLAYGPŢĠAĞKŢHŢMLĞSPEQPĠVĮ---PRALMDLLQLTREEGAEGRPWALSVTMSY 176
                                                                                                                                                                                                                                                                           230
                                                                                                                                                                                                                                                                                                                                          LEIYNEKIRDLLVQDPLSMEKPKSLNICEDAEQNVSVPGLSYFTPTNLEEVMEIIIRGNS 240
                                                                                                                                                                                                                                                                                                                                                                                 NRIVGATRINQRSSRSHAVILVKVDQRERLAPFRQREGK-----LYLIDLAGSED 280
                                                                                                                                                                                                                                                                                                                                                                                                     300 ASATKURĞKRLVEGANINRSLLALGUCINSLCE--PRRRQHVPYRDSKLTRLLKFSLGGN 357
                                                                                                                                  82
                                                                                                                                                             99
                                                                                                                                                                                              -----QETL-----KYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQ
                                                                                                                                                                                                                                                                                                                       LEIYQEKVLDLL--DPASGD----LVIREDCRGNILIPGLSQKPISSFADFERHFLPASR
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                                                                                                    16;
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                                                                      Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
28.3%; Score 532; DB 2; Length 12
Best Local Similarity 36.1%; Pred. No. 3.4e-34;
Matches 125; Conservative 74; Mismatches 113; Indels
                                                                    Query Match
28.5%; Score 536; DB 2; Length 78
Best Local Similarity 35.5%; Pred. No. 8.7e-35;
Matches 139; Conservative 61; Mismatches 116; Indels
                                                                                                                                44 VRVAVRLRPFVDGTAG--ASDPPCVRGMDSCSLEIANWRNH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHSILIANIAPERRFYLDTVSALNFAARSKEV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::| |:| :| |:| 389
CRTCMIVCISPSSEHYDETHNTLKYGNRAKNI 389
              SPDB:SPBC649.01c; SPDB:SPBC1685.15c
                                position: 2
                A,Gene: SPDB:SPI
A,Map position:
A,Introns: 11/1
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probable kinesin-related cytokinesis protein [imported] - Arabidopsis thaliana probable kinesin-related cytokinesis protein [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: H8477
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Accession: H8477
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: DNA
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                             A,Map position: 3
A;Introns: 113/2; 153/3; 194/3; 256/3; 330/3; 377/1; 427/1; 456/3; 527/3; 572/3; 632/3; C;Superfamily: kinesin-related protein KLP61F; kinesin motor domain homology F;124-466/Domain: kinesin motor domain homology <KMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ę,
                                                                                                                                                                                                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                            233 VRALEDIL-----LNASSASISVEISYLQLYMETIQDLLAPEKNNISINEDAKTGEVS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 VPGATVVNIQDLDHFLQVLQVGETNRHAANTKMNTESSRSHAILTVYVRRAMNEKTEKAK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCR-GNIL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 IPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKV-----DQRERLA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF------RQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----PEQPGVI 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM--LGSPE--QPGVI
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                                                                                                                                                                                                                                      Gaps
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A;Map position: 2
C;Superfamily: kinesin-related protein Eg5; kinesin motor domain homology
                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                             Length 1070;
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                                                                                                                                                                          28.0%; Score 525; DB 2; Length 10<sup>o</sup>35.3%; Pred. No. 1e-33;
tive 69; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.9%; Score 524; DB 2; Length 10
36.4%; Pred. No. 1.2e-33;
ive 67; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 QQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS----
                                                                                                                                                                                                                                Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 36.4*
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1056 <STO>
Gene: ATSP:F28P10.150
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
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                                                                                                                                                                                                                                                                                                                                                                                           Cidate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 16-Aug-2004
CiAccession: T30335
Riboleti, H.; Karsenti, E.; Vernos, I.
Cell 84, 49-59, 1996
A;Title: Xklp2, a new Xenopus centrosomal kinesin-like protein required for centrosome shreference number: 220827; MUID:96140639; PMID:8548825
A;Reference number: 220827; MUID:96140639; PMID:8548825
A;Accession: T30335
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1388 -BOL>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
Y106733
Kineain homolog F28P10.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: C3-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: C3-Apr-1999 #sequence_revision C3-Apr-1999 #text_change 09-Jul-2004
C;Date: C3-Apr-1999 #sequence_revision C3-Apr-1999 #text_change 09-Jul-2004
C;Date: C3-Apr-1999 #sequence Database, April 1999
A;Reference number: Z15793
A;Reference number: Z15793
A;Residues: L-1070 cQUBS
A;Residues: L-1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 VRVAVRLRPFVDGTAGASDPP---CVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP-----GVIPRA--- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |: :|: ||: : : : |
LFFLINREKEKAGEGKSFLCK--CSFIEIYNEQIFDLDSASAGLFLREHIKKGVFVVGA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 VEQVVISAAEAYQVLSMGWRNRRVASISMNRESSRSHAVFIVIIESMEKTNDLVNIRSSQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL----NQGLPRVPYRDSKL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                             LP2 protein - African clawed frog
.Species: Xenopus laevis (African clawed frog)
.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 16-Aug-2004
.Accession: T30335
                                                        LMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF-RQREGK
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                                                                                                                                         LGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                          Query Match 28.1%; Score 527.5; DB 2; Best Local Similarity 36.5%; Pred. No. 9.3e-34; Matches 126; Conservative 68; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: klp2
C,Superfamily: kinesin motor domain homology
                                                                                                                                         333
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PIDN: AAD24373.1; GSPDB:GNC

7;

DB 2; Length 1076;

71

225

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132 IFAYGQTGTGKTYTIMEGGARKKNGEIPSDAGVIPRAVKQIFDILEAQSAA----EYSLKV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRGMDSCSLBIA---NWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 VLTCNDRKKEVAVAQNIAGKQIDKTFLFBKVFGPTSQQXDLYHQAVSPIVFEVLDGYNCT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 TGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLAYGPTGAGKTHTMLGS-----PEQPGVIPRALMDLLQLTREEGAEGRPWALSVTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYLEIYQEKVLDLL------DPASGDLVIREDCRGNILIPGLSQKPISSFADFERHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 LPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ--REGKLYLIDLAGSEDNRR
                                                                                                                                                                                                                                                                                                                                                                                                                              6 STQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 EKGSAKRIAETLLNKQSSRSHSIFSVTIHIKECTPEGEEIVKSGKLNLVDLAGSENISR
A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: B84687
A,Status: preliminary
A,Rolecule 'type: DNA
A,Residus: 1-1076 <STO>
A,Cross-references: UNIPROT:Q9SIB3; GB:AE002093; NID:g4580395; PIDN:AAD243°
C,Genetics: A2228620
A,Genetics: A2228620
A,Hap position: 2
C,Superfamily: kinesin-related protein KIP1; kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.6%; Score 517.5; DB 2; Length llarity 32.6%; Pred. No. 4.1e-33; Conservative 74; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 NIAPERREYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::| :||:||:|| :| TVSPSVHCLEETLSTLDYAHRAKHIKN 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        126;
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Best Local S:
Matches 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinesin-related protein TKRP125 - common tobacco (Species: Nicotiana tabacum (common tobacco) (Species: Sc. Peb-1999 #sequence_revision 26-Peb-1999 #text_change 09-Jul-2004 (Spacession: T02017 (Spacession: T0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 INQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 LVEHLGHIPYRDSKLTRLLRDSLGGRTKTCIIATVSPAVHCLEETLSTLDYAHRAKNIKN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ASGDLV 196
                             252
                                                                               241
                                                                                                                                       KVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDA 310
                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 VRVAVRLRPFVDGTAGASDPPCVRGMD----SCSLEIANWRNHQETLKYQFDAFYGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PEQPGV
                             IREDCRGNILIPGLSQKPISS----FADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV
                                                                   tch 27.8%; Score 521.5; DB 2; Length 1006; al Similarity 35.6%; Pred. No. 1.8e-33; 128; Conservative 69; Mismatches 118; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOODIYAGSVOPILRHLLEGONASVLAYGPTGAGKTHTMLGS---
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Matches 128; Conserv
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: y, 7-11,59-64;125-132;222-226,'X',228-230 <COL2>
A; Residues: 2-5,'X', 7-11,59-64;125-132;222-226,'X',228-230 <COL2>
C; Complex: heterotrimer of a 115K chain and two kinesin-related chains of 95K (PIR:SS865 C; Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
F; Hy 1-348/Domain: kinesin motor domain homology <KMOT>
F; 11-348/Domain: kinesin motor domain homology <KMOT>
F; 97-104/Region: nucleotide-binding motif A (P-loop)
F; 103/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Reaidues: 1-699 <COL1>
A;Cross-references: UNIPROT:P46872; EMBL:L16993; NID:g295245; PIDN:AAA16098.1; PID:g2952
                                                                                                                                                                                                                                                                                                    eggs,
                                                                                                                                                                                                                                                                                   A,Title: Novel heterotrimeric kinesin-related protein purified from sea urchin A;Reference number: S18982; MUID:94050179; PMID:8232586 A;Accession: S18982
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Kinesin-related protein KRP85 - sea urchin (Strongylocentrotus purpuratus)
N,Alternate names: Kinesin-2 chain A; KRP (85/95) 85K chain
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S3982; S72531
R;Cole, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.; Scholey, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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37.6%; Pred. No. 3.9e-33;
iive 61; Mismatches 135;
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QQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLG---SPEQPGVIPRALMDLLQ 156
                                     44 VRVAVRLRPFVDGTAGASDPPCVRGMDSC--SLEIANWR--NHQETLKYQFDAFYGERST 99
         333 LGGSAHSILIANIAPERRYZLDTVSALNFAARSKEVIN 370 [||:|::|||| | :|:|| | :| :| | 307 LGGNAKTVMCANIGPAEYNYDETISTLRYANRAKNIRN 344
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Search completed: November 5, 2004, 18:45:31 Job time : 12.7872 secs

Ivis bade plank (nsbto)

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SEQ ID NO 259
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Sequence 4, Appli
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Sequence 2, Appli
Sequence 19691, A
Sequence 19691, A
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                                                                                                                             5, 2004, 18:38:46; Search time 5.60933 Seconds (without alignments) 1056.470 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                     US-10-797-893-2
1878
1 MAAGGSTQQRRREWAAASAA......FYLDTVSALNFAARSKEVIN 370
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(cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

(cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-948-973-4
US-10-948-973-4
US-10-951-582-4
US-10-951-582-6
US-10-951-582-8
US-10-951-582-8
US-10-220-366A-19691
US-10-220-366A-19691
US-10-220-366A-19691
US-10-220-366A-19691
US-10-732-923-6842
US-10-732-923-6842
US-10-732-923-6845
US-10-732-923-6846
US-10-732-923-6846
US-10-732-923-6846
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US-10-732-923-6751
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                                                                                                                                                                                                                                                                                                                                                                                     67802 segs, 16016457 residues
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                                                                                       OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length D
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App	Αp	Ap	4	Ap	Ap	Ap	Ap	Αp											
424,	7145,	7146,	7147,	7148,	7149,	6852,	6770,	7188,	7198,	7199,	6853,	6855,	6856,	10271	7200,	6936,	6973,	6857,	6858,
Sequence	Sequence	Sequence	Seguence	Sequence	Sequence		Sequence			Sequence			Sequence	Sequence	Seguence			Sequence	Sequence
US-10-732-923-424	US-10-732-923-7145	US-10-732-923-7146	US-10-732-923-7147	US-10-732-923-7148	US-10-732-923-7149	US-10-732-923-6852	US-10-732-923-6770	US-10-732-923-7188	US-10-732-923-7198	US-10-732-923-7199	US-10-732-923-6853	US-10-732-923-6855	US-10-732-923-6856	US-10-732-923-10271	US-10-732-923-7200	US-10-732-923-6936	US-10-732-923-6973	US-10-732-923-6857	US-10-732-923-6858
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912	912	912	912	912	915	912	852	865	875	846	606	918	918	361	900	839	878	918	918
5.1	5.1	5.1	5.1	5.1	5.1	2.0	5.0	5.0	5.0	4.9	4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7
95	. 95	95	95	95	92	94.5	94	93.5	93	92.5	91	90.5	90.5	90	89.5	88.5	88.5	88.5	88.5
36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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39.7%; Pred. No. 1.1e-43;
ive 59; Mismatches 114; Indels 41; Gaps
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                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ITOH, KYOSO
TITLE OF INVENTION: TUMOR ANTIGEN
FILE REFERENCE: Q-70382
CURRENT APPLICATION NUMBER: US/10/734,049A
CURRENT FILING DATE: 2003-12-12
PRIOR APPLICATION NUMBER: PCT/JP02/05799
PRIOR FILING DATE: 2002-06-11
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 408
SOFTWARE: PATENTIN VERSION 3.3
ALIGNMENTS
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Best Local Similarity 39.7%
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-734-049A-259
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                                                                                                                                                                                                                                                                                                                                                                                     88 -----YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTML- 138
                                                                                                                                                                                                                                                                                                                                                                                                                              61 PAPPTRHDFSFDRVFPPGSGQDBVFE-EIAMLVQSALDGYPVCIFAYGQTGSGKTFTMEG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 VLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGL-----RLKESGAINTS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 LSTLGLVIMALSNKESHVPYRNSKLTYLLQNSLGGSARMLMFVNISPLEENVSESLNSLR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 ---GSPEOPGVIPRALMDLLQLTREEGAEGRPWALSVTWSYLEIYOEKVLDLLDPAS--- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
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7 IRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPP-----TRLSLSRSDERRGTLSGA
                                                                                                                                                                                                                                                         ----FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK--
                                                                                                                                                                                                                                                                                                                       8 IRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPP----TRLSLSRSDERRGTLSGA
                                                                                                                                                                                            Gaps
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                                                                                                                           Length 361;
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general INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1043
CURRENT APPLICATION NUMBER: US/10/948,973
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: US/10/126,205
PRIOR APPLICATION NUMBER: US/10/126,205
PRIOR APPLICATION NUMBER: US/09/723,595
PRIOR APPLICATION NUMBER: US/09/723,595
PRIOR APPLICATION NUMBER: US/09/723,595
PRIOR PELING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/723,595
PRIOR PELING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/295,612
PRIOR PELING DATE: 1000-11-28
PRIOR PERIOR DATE: 1000-11-28
PRIOR PERIOR DATE: 2000-11-28
PRIOR PERIOR DATE: 2000-11-28
PRIOR PERIOR DATE: 2000-11-28
PRIOR PERIOR DATE: 2000-11-28
                                                                                                                       Score 423, DB 6; Length 36.
Pred. No. 4e-32;
9; Mismatches 131; Indels
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                                                                                                                              22.5%; Scoi
32.8%; Prective 59; 1
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Best Local Similarity 32.8
Matches 121; 'Conservative
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                             44 VRVAVRLRP-----
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                                                                                                                                                                    Similarity
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                                  Human
                                                                                                                              Query Match
Best Local Simi
Matches 121;
; TYPE: PRT
; ORGANISM: Hur
US-10-948-973-2
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Sequence 164, Application US/10952698

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mack, David
APPLICANT: Aziz, Natasha
TITLE OF INVENTION: OF SCREENING FOR MODULATORS OF BLADDER CANCER
TITLE OF INVENTION: OF SCREENING FOR MODULATORS OF BLADDER CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/952,698
CURRENT FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin version 3.2
SEQ ID NO 164
FURTHER OF SECOND ON 164
FURTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 VRVAVRLRPFVD--GTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 DIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP-----GVIPRA---L 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 MDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLS 211
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                                               ---HPYRNSKLTRLLKDSLGGNCQTIMIAAVSPSSVFYDDTYNTLKYANRAKDI 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.0%; Score 526; DB 6; Length 1380; 37.2%; Pred. No. 6.3e-41; ive 66; Mismatches 128; Indels 2
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SEQUED CO. 2. Application US/10948973

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: their use

FILE REFERENCE: 1043

CURRENT APPLICATION NUMBER: US/10/948,973

CURRENT PILING DATE: 2004-09-24

FRIOR APPLICATION NUMBER: US/10/126,205

PRIOR APPLICATION NUMBER: US/09/723,595

FRIOR FILING DATE: 2000-11-28

FRIOR FILING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FREEEE (FOR WINDOWN VERSION 4.0)

SEQ ID NO 2

LENGTH: 361
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Best Local Similarity 37.24
Matches 128; Conservative
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 PRCLDMIFNSIGSFQAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQVD 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 ERLAP-----FRQRE----GKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 KVVDALNQGL-----PRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 494;
                                                                                                                                                              APPLICANT: Valaberg, Eugeni
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: Their use
FILE REFRENCE: 1041
CURRENT APPLICATION NUMBER: US/10/951,582
CURRENT APPLICATION NUMBER: US/10/143,563
PRIOR APPLICATION NUMBER: US/209-773,630
PRIOR APPLICATION NUMBER: US/209-723,630
PRIOR APPLICATION NUMBER: US/209-6-19
PRIOR APPLICATION NUMBER: US/209-723,630
PRIOR PILING DATE: 2000-6-15
PRIOR PILING DATE: 1999-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.0%; Score 394; DB 6; L 27.3%; Pred. No. 3.3e-29; ive 64; Mismatches 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                            US-10-951-582-4; Sequence 4, Application US/10951582; GENERAL INFORMATION:
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Best Local Similarity 27.34
Matches 117; Conservative
                          353 FASKVNQCV 361
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FAEVTQEV
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US-10-951-582-6
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                    PAPPTRHDFSFDRVFPPFGSGQDEVFB-EIAMLVQSALDGYPVCIFAYGQTGSGKTFTMEG 119
---GSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPAS--- 192
                                                                      --GDLVIREDCRGN--ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHA 248
                                                                                                                                                  --RLKESGAINTS 300
                                                                                                                                                                                                                     LFVLGKVVDALNOGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
                                                                                                                                                                                                                                        292 LSTLGLVIMALSNKESHVPYRNSKLTYLLQNSLGGSAKMLMPVNISPLEENVSESLNSLR 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 ---GSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVIMSYLEIYQEKVLDLLDPAS--- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GPGGDPQLEGLIPRALRHLFSVAQELSGQG--WTYSFVASYVEIYNETVRDLLATGTRKG 177
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IRVPCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPP-----TRLSLSRSDERKGTLSGA
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10948973
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and methods for
FILE REPERENCE: 1043
CURRENT APPLICATION UNMBER: US/10/948,973
CURRENT APPLICATION NUMBER: US/10/126,205
FRIOR APPLICATION NUMBER: US/10/126,205
PRIOR PILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR PILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                             VLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGL-----
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FASKVNQCV 360
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ORGANISM: Human
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US-10-948-973-4
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Query Match
Best Local Similarity 27.29
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 FAEVTOE 433
                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                     LENGTH: 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 PEFADMITVQEFCKABEVDEDSVYGVFVSYIBIYNNYIYDLLEEVPFDPIKPRPPQSKLL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 ERLAP-----FRORE----GKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 KVVDALNQGL----PRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 TCMDVLRENOMYGTNKAVPYRDSKLTHLFKNYFDGEGKVRMIVCVNPKAEDYEENLOVMR 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----MD-----ILLQLTREEGAEGRPWALS---- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VTMSYLEIYQEKVLDLLDPASGDLV------ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 VGVYCRVRPL----GPPD-----QECCIEVINNTIVQLHTPEGYRLNRNGDYKET-Q 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIAN------WR-----NHOETLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
21.0%; Score 394; DB 6; Length 658;
Best Local Similarity 27.3%; Pred. No. 5e-29;
Matches 117; Conservative 64; Mismatches 127; Indels 12
    GENERAL INFURCANILOW:

GENERAL INFURCANIT: Valsberg, Eugeni
APPLICANIT: Wood, Kenneth
APPLICANIT: Wood, Kenneth
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1041
CURRENT APPLICATION NUMBER: US/10/951,582
CURRENT PILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/09/723,630
PRIOR APPLICATION NUMBER: US/09/723,630
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 6
I TENNETH FARENCE OF WINDOWS VETSION 4.0
SEQ ID NO 6
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GENERAL INFORMATION:
APPLICANT: Valaberg, Eugeni
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1041
CURRENT APPLICATION NUMBER: US/10/951,582
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GENERAL INFORMATION:
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ORGANISM: Human
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88 YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 VGVYCRVRPL-----GPPD-------QECCIEVINNTTVQLHTPEGYRLNRNGDYKET--Q 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 PEFADMITVQEFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLLEEVPFDPIKPKPPQSKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 REDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIAN------WR----NHQETLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 433;
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APPLICANT: Wood, Kenneth
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Howel motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1041
CURRENT APPLICATION UNMBER: US/10/951,582
CURRENT APPLICATION NUMBER: US/10/143,563
PRIOR APPLICATION NUMBER: US/09/723,630
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-65-09
PRIOR FILING DATE: 2000-66-15
PRIOR APPLICATION NUMBER: US/95/944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.8%; Score 390; DB 6; 27.2%; Pred. No. 6.5e-29; iive 64; Mismatches 127;
CURRENT FILING DATE: 2004-09-27

PRIOR APPLICATION NUMBER: US/10/143,563

PRIOR FILING DATE: 2002-05-09

PRIOR APPLICATION NUMBER: US/09/723,630

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-06-15

PRIOR PRILING DATE: 2000-06-15

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1999-05-18

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10951582
GENERAL INFORMATION:
APPLICANT: Vaisberg, Eugeni
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172 VTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRN 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :|| |||||||| DEVFGEACTNQDVYMKTTHPLIQHIFNGGNATCFAYGQTGAGKTYTMIGTHENPGLYALA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 VSMDYLEIDSEMIRDLLNTFPVHLELQQDSSGVIQGAGITEASTINAKEIMHLLMKGNRQ 77
      76 LALINVLNALADAKGRKTHVPYRDSKLTRLLKDSLGGNCRTVMIAAISPSSMTNEDTYS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 RIVGATRINQRSSRSHAVLLVKVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRIGN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 PAR----VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY-----QF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.7%; Score 183; DB 6; Length 134; 40.2%; Pred. No. 2.9e-10; iive 19; Mismatches 49; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.6%; Score 180; DB 6; Length 134; Best Local Similarity 33.3%; Pred. No. 5.6e-10; Matches 42; Conservative 21; Mismatches 53; Indels
                                                                                                          GENERAL INFORMATION:

GENERAL INFORMATION:

TOTLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICANT:

CURRENT APPLICATION NUMBER: US/10/20,366A

CURRENT APPLICATION NUMBER: US/10/20,366A

CURRENT PILING DATE: 2002-08-28

PRIOR PILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 27802

SOFTWARE: CUSCOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
FURENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i LOCATION: (1) ... (134)
i OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-14894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 26476, Application US/10220366A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-220-366A-26476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                        RESULT 11
US-10-220-366A-14894
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US-10-220-366A-26476
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SEQ ID NO 26476
LENGTH: 134
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LENGTH: 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 CSLEIAN-----WR----NHQBŢLKYQFDAFYGERSŢQQDIYAGSVQPILRHL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 SYLEIYQEKVLDLL-----DPASGDLVIREDC-----RGNILIPGLSQKPISSFADFERH 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 SYIEIYNNYIYDLLEEVPPDPINPNL-HNLNCFVKIKNHNMYVAGCTEVEVKKSTEEAFEV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLPASRNRTVGATRINQRSSRSHAVILVKVDQRERLAP-----FRQRE----GKLYL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGL----PRVPYRDSKLTR 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 SRSHAVLLVKVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL 301
                                                                                                                                                                                                                                                                                                                       16 SGTHAVFQFFLKQQGRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 FVLGKVVDALNQGLPR---VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVS 357
                                                                                                                                                                                                 Query Match
19.8%; Score 371; DB 6; Length 960;
Best Local Similarity 27.4%; Pred. No. 1.3e-26;
Matches 110; Conservative 63; Mismatches 118; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    116 LEGONASVLAYGPTGAGKTHTMLGSPEQPGVIPRAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 19691, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: NOVE:
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR PILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: | :: | :: | 394 LPKNYFDGEGKVRMIVCVNPKAEDYEENLQVMRFAEVTQEV 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 MD-----LLQLTREEGAEGRPWALS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 206.5; DB 6;
46.2%; Pred. No. 1.9e-12;
tive 15; Mismatches 44;
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 960
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Matches 55; Conserv
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US-10-220-366A-19691
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                                                                                                                                  ORGANISM: Human
                                                                                                                                                           US-10-951-582-8
                                                                                                               TYPE: PRT
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Gaps

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RESULT 15
US-10-732-923-6842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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6.0%; Score 113; DB 6; Length 911;
Best Local Similarity 21.4%; Pred. No. 0.018;
Matches 83; Conservative 69; Mismatches 128; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2003-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 6841
                                                                                         Sequence 15821, Application US/10220366A

Sequence 15821, Application US/10220366A

GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REPERENCE: 12172-042
CURRENT APPLICATION NUMBER: US/10/220,366A

CURRENT APPLICATION NUMBER: 09/577,409
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: Custom
SEQ ID NO 15821
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 139;
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                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1).7.(139)
; OTHER INFORMATION: Xaa = any amino acid or nothing US-10-220-366A-15821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 SAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.3%; Score 174; DB 6; Best Local Similarity 43.2%; Pred. No. 2.1e-09; Matches 41; Conservative 17; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana US-10-732-923-6841
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                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
151 LMDLLQ 156
                           121 AKDIFR 126
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US-10-732-923-6841
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6.0%; Score 113; DB 6; Length 911;
Best Local Similarity 21.4%; Pred. No. 0.018;
Matches 83; Conservative 69; Mismatches 128; Indels 108; Gaps
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Sequence 6842. Application US/10732923
GENERAL INFORMATION
TITLE OF INVENTION: TRANSGENCE PLANTS WITH IMPROVED PHENOTYPES
TITLE REPERENCE: 38-15.52796.C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
FRIOR FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
NUMBER: OF SEQ ID NOS: 24149
SEQ ID NO 6842
LENGTH: 911
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                ETLKYQFDAFYGERSTQQDIYAGSVQPIL--
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; ORGANISM: Arabidopsis thaliana
US-10-732-923-6842
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Search completed: November 5, 2004, 19:04:48 Job time : 6.60933 secs

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288.
528
526
526
   14
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1878
1 MAAGGSTQQRRREMAAASAA......FYLDTVSALNFAARSKEVIN
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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/cgn2_6/ptcdata/2/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US60_NEW_PUB.pep:*
                              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Result Ouery No. Score Match Length DB ID Description

1 1878 100.0 370 16 US-10-797-893-2 Sequence 2, Appli 2 1878 100.0 490 15 US-10-797-893-6 Sequence 80, Appli 3 1873 99.7 512 16 US-10-797-893-6 Sequence 6, Appli 5 US-10-797-893-6 Sequence 1228, Appli 6 1763 93.9 460 9 US-09-925-300-1228 Sequence 1228, Appli 6 1763 93.9 487 16 US-10-797-893-6 Sequence 1228, Appli 7 US-10-128 Sequence 1529, Appli 8 597.5 31.8 37 16 US-10-797-893-8 Sequence 15293, Appli 1 US-10-425-115-32029 Sequence 2652, Appli 1 US-10-425-115-332919 Sequence 332919, 1 1 557.5 29.7 781 17 US-10-425-115-332919 Sequence 59708, Appli 1 S57.5 29.0 776 16 US-10-425-114-59708 Sequence 59708, Appli 1 S58 28.1 381 9 US-09-883-096-5 Sequence 5, Appli

121 ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIY 180

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	Sequence 106, App Sequence 112, App Sequence 1177, Ap Sequence 116714, Sequence 102, App Sequence 2153, Ap Sequence 2153, Ap Sequence 2153, Ap Sequence 214, App Sequence 214, App Sequence 214, App Sequence 21903, Ap Sequence 21, Appli Sequence 1164, Ap Sequence 1164, Ap Sequence 1164, App Sequence 117, Appli Sequence 117, Appli Sequence 118, Appli Sequence 118, Appli Sequence 664, App Sequence 664, App Sequence 664, App Sequence 664, App	. for	; Length 370; indels 0; Gaps 0; PPARVRVAVRLRPPVDGTAGA 60
08-0 08-0 08-0 08-0 08-0 08-0 08-0	5 US-10-287-226-306 5 US-10-425-1142 6 US-10-408-765A-1477 6 US-10-408-765A-1477 6 US-10-408-765A-137671 5 US-10-287-26-302 4 US-10-116-712-670 6 US-10-287-226-314 7 US-10-334-143-38 7 US-10-334-143-33 6 US-10-349-321903 7 US-10-349-321903 8 US-10-408-765A-1664 US-10-458-162-1 4 US-10-458-162-1 4 US-10-458-162-1 4 US-10-468-123-14 6 US-10-10-685-112-4 7 US-10-16-712-664 7 US-10-116-712-664 7 US-10-116-712-664	ALIGNMENTS 797893 74.1 te cor proteins and methods see (2010/797,893 (209/724,224 8) (209/724,224 8) (209/724,224 8) (209/729) (200/7597,292 6	; Score 1878; DB 16 ; Pred. No. 4.3e-177 0; Mismatches 0; AAAISGAGRCRLSKIGATRRP AAAISGAGRCRLSKIGATRRP NRHQETLKYQFDAFYGERSTR NRHQETLKYQFDAFYGERSTR
8.0 8.0 8.0 8.0 8.0 9.0 1388	27.9 1834 27.7 1826 27.7 1826 27.7 1826 27.6 1138 27.6 1138 27.6 1232 27.6 1232 27.6 1232 27.5 1324 27.5 1324 27.1 1232 27.2 1672 27.2 1672 27.0 928 27.0 928 27.0 1232 27.0 1232 27.0 1232 27.0 1232 27.0 1232	Application US/1079 Application US/1079 NEWATION: Beraud, Christophe WENTION: Novel moto VENTION: Novel moto NUCE: 1044 ILICATION NUMBER: US/0 CATION NUMBER: US/0 CATION NUMBER: 09/5 CATION NUMBER: 09/5 GD DATE: 2000-11-28 GC DATE: 2000-11-28 GC DATE: 2000-11-28 GC DATE: 2000-10-6-20 GEO DATE: 2000-06-20 GEO DATE: 2000-06-20 HUMBAN	100.0\$ imilarity 100.0\$); Conservative MAAGGSTQQRRREMAAAS;
50000000000000000000000000000000000000	25 523.5 27 521.5 28 519.5 29 518.5 30 518.5 31 518 33 518.5 34 517.5 35 516 36 510 38 510 40 509 41 507 42 507 43 507	RESULT 1 Sequence 2, Application US/10 Fublication No. US2040142397, Fublication No. US2040142397, Fublication No. US2040142397, TITLE OF INVENTION: Novel more TITLE OF INVENTION: Novel more TITLE OF INVENTION: UNBER: CURRENT APPLICATION NUMBER: CURRENT PILIMS DATE: 2004-06-2, PRIOR PILING DATE: 2000-11-2, PRIOR PELICATION NUMBER: USPRIOR FILING DATE: 2000-06-2, NUMBER OF SEQ ID NOS: 8 SOFTWARE: FREESEQ for WINGOM; SEQ ID NO 2 LENGTH: 370 LENGTH: 370 TYPE: PRT ORGANISM: Human US-10-797-893-2	Query Match Best Local Simila Matches 370; Cc Oy 1 MAAG Oy 1 MAAG Oy 61 SDPP Ob 61 SDPP

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                                         240
                                                        ORSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS 300
                                                                                                                                                       LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
           ASVLAYGPTGAGKTHTMLGSPEQPGVÍPRALMDLLQLTREEGAEGRPWALSVTMSYLEIY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA 68
                                                                                                                                                                                                                                                                                                          Sequence 80, Application US/10334143
; Sequence 80, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
    APPLICANT: GENIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: MINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT PRILING DATE: 2002-12-31
; PRIOR PILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PATCHIN Ver. 2.1
; SEQ ID NO 80
                                                                                                                241 QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS
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                                         QEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLN
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Length 490;
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ORGANISM: Homo sapiens
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US-10-334-143-80
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US-10-334-143-80
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; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REPERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-16-28
; PRIOR FILING DATE: 2000-16-28
; PRIOR FILING DATE: 2000-16-28
                                                                                                       methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.7%; Score 1873; DB 16;
100.0%; Pred. No. 2.2e-176;
iive 0; Mismatches 0;
      Sequence 4, Application US/10797893

Publication No. US20040142397A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Novel motor proteins and met;
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION UNMERR: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR FILING DATE: 2004-03-09
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
LENGTH: 512
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Best Local Similarity 100.
Matches 369; Conservative
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US-10-797-893-4
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US-10-797-893-4
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PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG 203
                                                                                                                                                                                   182 NILIPGLSQXPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVXVDQRERLAPF 241
                                                                                                                                                                                                                                                                                                                            242 RQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDS 301
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                                                                                             ETLKYOFDAFYGERSTOODIYAGSVOPILRHLLEGONASVLAYGPTGAGKTHTMLGSPEQ
                         GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQ
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                                                                                                                                                                                                                                                                                                       ROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDS
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US-10-797-893-8

US-10-797-893-8

Sequence 8, Application US/10797893

Publication No. US20040142397A1

GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 104

CURRENT FILING DATE: 2004-03-09

PRIOR FILING DATE: 2004-01-09

PRIOR FILING DATE: 2000-01-128

PRIOR FILING DATE: 2000-01-29

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEVOID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%; Pred. No. 1.6e-165; Matches 345; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 487
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                                                                                                                                                                                                                                                                                  86 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                              265
                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                      62 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
                                                                                                                                                                                                                                                                                                                                                                             REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                              26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                    2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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                                                                                                                                              Length 346;
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; Sequence 1228. Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REPERBNES: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR PILING DATE: 1909-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.9%; Score 1763; DB 9; Length 460; 99.4%; Pred. No. 1.5e-165; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                          93.9%; Score 1763; DB 16;
100.0%; Pred. No. 9.7e-166;
iive 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (75)
OTHER INFORMATION: Xaa equals any
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xaa equals any
                                                                                                                                         Query Match 93.9
Best Local Similarity 100.
Matches 345; Conservative
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Best Local Similarity 99.4
Matches 345; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (435)
; OTHER INFORMATION:
US-09-925-300-1228
                                                                                    , ORGANISM: Human
US-10-797-893-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-925-300-1228
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NAME/KEY: SITE
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 159031
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 --YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPBQPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 VIPRALMDILQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 LMXSTVLALCTGT------WC-SVEISYYEVYMERCYDLLEPKAREIMVLDDKDGNL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 REGKLYLI---DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRD 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 RVRVAVRLRPP--VDGTAGAS-----DPPCVRGMDSCSLEIANWRNHQETLK-YQPDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 39.7%; Pred. No. 3.7e-50;
Matches 138; Conservative 69; Mismatches 112; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 SKITRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; sequence 2692, Application US/10108260A; sequence 2692, Application Wo. US20040005560A1; Publication Wo. US20040005560A1; GENERAL INFORMATION:
; APPLICANT: HIBLIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; CURRENT PILIACATION NOMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 2692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
29.8%; Score 559; DB 15; Length 548;
Best Local Similarity 38.9%; Pred. No. 4.2e-46;
Matches 132; Conservative 70; Mismatches 121; Indels 16
                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_58448C.1.pep
US-10-437-963-159031
                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(377)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-108-2608-2692
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
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US-10-425-115-320209

US-10-425-115-320209

Sequence 320209, Application US/10425115

Sequence 320209, Application No. US20040214272A1

Septication No. US20040214272A1

SETILGANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: APPLICANT: And Molecules and Other Molecules Associated With

TITLE OF INVENTION: Noleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Noleic Acid Molecules

FILE REFERENCE: 38-21 (5320)

CURRENT APPLICATION NOMBER: US/10/425,115

CURRENT APPLICATION NOMBER: US/10/425,115

SEQ ID NO 322209

LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSH 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 AVLSLRVSSTDVV-----KGKLNLIDLAGSEDNKRTLNEGIRLQESSKINQSLFALSNV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 VDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 PGGGVIVQLKD-QHISKSEQYKLDAFFRQEDSVSQIFDQEVRAVIPSIFEGINATVFAYG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 PTGAGKTHTMLGSPEOPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 AIGSGKTYTMGGTEDFPGLIPLAASTILALCT----GTWC-SVEISYYEVYMERCYDL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 ----SLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 MAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.0%; Score 601; DB 17; Length 58: 39.1%; Pred. No. 3.2e-50; Live 72; Mismatches 113; Indels
                               TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                       302 TRILQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_55097C.1.pep
US-10-425-115-320209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 159031, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 39.1
Matches 142; Conservative
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US-10-437-963-159031
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APPLICANT: Zhou, Yihuan APPLICANT: Zhou, Yihuan APPLICANT: Zhou, Yihuan APPLICANT: Kovalit, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement TITLE REPERENCE: 38-21(53313)8
CURRENT APPLICANTION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                466 LLALSSCINALVEGKKHIPYRNSKLTQLLKDSLGGACNTVMIANISPSNLSFGETQNTLH 525
LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 RKLSLGGAVGGKLKAAG----EVGAGTAEAAESRILVFVRLRPMSRKEKEAGSRSCVKI 305
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US-10-425-114-59708
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                              ; Sequence 59708, Application US/10425114; Publication No. US20040034888A1 ; GENEAL INFORMATION: APPLICANT: Liu, Jingdong
                                                                                                              FAARSKEV 368
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526 WADRAKEI 533
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exovalic, David K.
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 332919
LENGTH: 783
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                                                  154 LLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK 213
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OTHER INFORMATION: unsure at all Xaa locations
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APPLICANT: Craven, Andrew
APPLICANT: Craven, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Bakowicz, Roman
APPLICANT: Parel, Umesh A.
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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INTER: 383

LENGTH: 383

LENGTH: 383

CRGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HsKip3a

OTHER INFORMATION: fragment

OTHER INFORMATION: the Annio acid sequence of HsKip3a fragment used other INFORMATION: the ATPase assay (Figure 4).
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28.1%; Score 528; DB 9; Length 864;
Best Local Similarity 38.7%; Pred. No. 9.7e-43;
Matches 138; Conservative 46; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.1%; Score 528; DB 9; Length 38:
38.7%; Pred. No. 2.9e-43;
tive 46; Mismatches 127; Indels
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ORGANISM: Artificial Sequence
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Matches 138; Conservative
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LENGTH: 864
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APPLICANT: Li, Ping
TITLE DE INVENTION: Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53211)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDPPCVRGMDSCSLEIANWRNHQETLK-----YQFDAFYGERSTQQDIYAGSVQPIL 112
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; Sequence 5, Application US/09883096
; Patent No. US20020110883A1
; GENERAL INFORMATION:
; APPLICANT: Braad, Christophe
; APPLICANT: Sakowicz, Roman
; APPLICANT: Sakowicz, Roman
; APPLICANT: Patel, Umesh A.
; APPLICANT: Patel, Umesh A.
; APPLICANT: Davies, Katherine A.
; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
; TILE REPRENCE: 02052-001410US;
; TILE REPRENCE: 02052-001410US;
; PRIOR PPLICATION NUMBER: US/09/883,096
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                          Wu, Wei
Boukharov, Andrey A.
                    Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
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Matches 133; Conservative
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US-10-437-963-103943
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US-09-883-096-5
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Query Match

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FEATURE:

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271 YLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL----NQGLPRVPYRDSKLT 326
                                              262 NLVDLAGSERQKDTHAEGMRLKEAGNINRSLSCLGQVITALVDVGNGKQRHVCYRDSKLT 321
                                                                                                                                                        RILQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                           322 FLLRDSLGGNAKTAIIANVHPGSRCFGETLSTLNFAQRAKLIKN 365
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US-10-332-089-4
                                                                                                                                                                                                                               137 MLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLV 196
                                                                                                                                                                                77 ANWRNHOETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHT 136
                                                                                                                                                                                                                                                                                                                                                                               197 IREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQ 256
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                                       ---TAGASDPPCVRGMDSCSLEI 76
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                                                                                             15 RPPTPRELDSQR-RPVVQVVDERVLVFNPEEPDGGFPGLKWGGTHDGPKKKGKD----
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Fublication No. US20040072175A1
FORDRAL INFORMATION:
APPLICANT: Stand, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Sakovicz, Roman
APPLICANT: Wood, Kenneth WO.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/10/332,089
CURRENT FILING DATE: 2002-12-17
FRIOR APPLICATION NUMBER: WO PCT/US01/16300
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VOYE: 2.1
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Best Local Similarity 37.2%; Pred. No. 4.5e-43;
Matches 128; Conservative 66; Mismatches 128;
                                   RPPPARVRVAVRLRPFV-
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ORGANISM: Homo sapiens
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November 5, 2004, 18:44:52 ; Search time 58.709 Seconds (without alignments) 2081.726 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:-
/ cgn2_6/ptodata/2/pubpaa/NEO7_NEW_PUB.pep:-
/ cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:-
/ cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:-
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/ptodata/2/pubpaa/US06_NEW_PUB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/PCTUS_E
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 6, Appli	Sequence 8, Appli	Sequence 2. Appli	Seguence 80, Appl	Sequence 4. Appli	Sequence 1228, Ap	Sequence 159031.	Sequence 320209.	Sequence 2692, Ap	Sequence 332919,	Sequence 59708. A	Sequence 103943.	Sequence 5, Appli
		ai	US-10-797-893-6	US-10-797-893-8	5 US-10-797-893-2	US-10-334-143-80	US-10-797-893-4	US-09-925-300-1228	US-10-437-963-159031	US-10-425-115-320209	US-10-108-260A-2692	US-10-425-115-332919	US-10-425-114-59708	US-10-437-963-103943	US-09-883-096-5
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		Match Length DB	346	487	370	490	512	460	377	589	548	783	854	116	383
من	Query	Match	100.0	100.0	99.7	7.66	99.7	99.2	33.8	33.6	31.6	31.1	31.1	30.4	29.9
		Score	1768	1768	1763	1763	1763	1753	597.5	593.5	559	550	550	537	528
	Result	No.	-	7	m	4	2	9	7	89	თ	10	11	12	13

Sequence 2, Appli Sequence 366, App Sequence 316, App Sequence 4, Appli Sequence 6, Appli	.,	30 41 71	Sequence 310, App Sequence 670, App Sequence 2153, Ap Sequence 8, Appli Sequence 231231, Sequence 314, App	ירפטטטן	Sequence 1, Appli Sequence 13, Appl Sequence 112, App Sequence 664, App Sequence 669, App Sequence 669, App
) US-09-883-096-2 IS US-10-220-120-366 IS US-10-333-829-316 IS US-10-332-089-4 IS US-10-332-089-6	-sn -sn -sn -sn	US-10 US-10 US-10 US-10	US-10 US-10 US-10 US-10 US-10	US-10 US-10 US-10 US-10 US-10	4 US-10-458-1628 4 US-10-080-608 4 US-10-370-685 4 US-10-116-712 4 US-09-883-096-
864 757 757 375 409	774 1388 1388 1388 1388	834 1 1401 1 1826 1			1103 1103 1232 1232 1232 1338 9
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ALIGNMENTS

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	6; 0; Gaps			
	346;	LEIA	THTMI 	DLVI
for	Length 346; Indels 0;	VRGMDSCS	YGPTGAGK	DLLDPASC
ULT 1 10-797-893-6 equence 6, Application US/10797893 ublication No. US20040142397A1 EMERAL INFORMATION: APPLICANT: Beraud, Christophe TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use FILE REPERENCE: 1044 CURRENT APPLICATION NUMBER: US/10/797,893 CURRENT FILING DATE: 2004-03-09 PRIOR PTLING DATE: 2000-11-28 PRIOR PELIOR TOWNINGER: US/09/724,224 PRIOR FILING DATE: 2000-06-20 RIOR FILING DATE: 2000-06-20 RUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 6 LENGTH: 346 TYPE: PRT ORGANISM: Human		MGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQE 	TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP	EIYQEKVL
ins and , 893 24 4.0	Score 1768; DB 16; Pred. No. 1.7e-168; Mismatches 0;	RPFVDGTZ RPFVDGTZ	ILRHLLEC	SVTMSYLI
ULT 1 10-797-893-6 equence 6, Application US/10797893 ublication No. US20040142397A1 ERNERAL INPORMATION: TITLE OF INVENTION: Novel motor proteins TITLE OF INVENTION: their use FILE REFERENCE: 1044 CURRENT APPLICATION NUMBER: US/10/797,893 CURRENT FILING DATE: 2004-03-09 PRIOR FILING DATE: 2000-11-28 PRIOR APPLICATION NUMBER: US/9724,224 PRIOR FILING DATE: 2000-11-28 PRIOR SEQ ID NOS: 8 SOFTWARE: FastESQ for Windows Version 4.0 EQ ID NO 6 EMOTOR 1346 TYPE: RATE ORGANISM: Human 10-797-893-6	ä	GATRRPPPARVRVAVRLRPE	YAGSVQP	EGRPWAL
nn US/1079 (0142397A1 rristophe lovel moto: their use 2004-03: 2004-03: 108RR: US/09 108-09/5: 00-06-20	, , , ,	REPPAR	STOODI	TREEGA
SULT 1 -10-79-893-6 -10-79-893-6 Sequence 6, Application US/10797893 Publication No. US20040142397A1 GENERAL INFORMATION. APPLICAT: Beraud, Christophe TITLE OF INVENTION: Novel motor prot- TITLE OF INVENTION: their use FILE REFERENCE: 1044 CURRENT FILING DATE: 2004-03-09 PRIOR APPLICATION NUMBER: US/09/724, PRIOR RILING DATE: 2000-11-28 PRIOR FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Versio: 3070-10-30 SOFTWARE: FastSEQ for Windows Versio: 2000-10 NO 6 LENGTH: 346 TYPE: PRT ORGANISM: Human	/at	SKIGATE SKIGATE	DAFYGER	LMDLLQI
-6 No. US ORMATIC ORMATIC NVEN	Similar S; Con	MGRCRI MGRCRI		GVIPRA
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NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 490
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-797-893-2
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Best Local Simi:
Matches 345; (
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100.0%; Score 1768; DB 16; Length 487;

Best Local Similarity 100.0%; Pred. No. 2.8e-168;

Matches 346; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                          Sequence 2, Application US/10797893 Publication No. US20040142397A1 GENERAL INFORMATION:
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US-10-797-893-8
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US-10-797-893-2
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Sequence 80, Application US/20040009549A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GENCORIEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543
CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT PILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR FILING DATE: 2001-12-31
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 370
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99.7%; Score 1763; DB 15;
Best Local Similarity 100.0%; Pred. No. 9e-168;
Matches 345; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.9e-168;
tive 0; Mismatches 0;
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LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-09-925-300-1228
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                                                                                                           Sequence 1228, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
TEAST STORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAU OF TOWNER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
CURRENT FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFFWARE: PATENTIN VEY: 2.0
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 302 TRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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ORGANISM: Homo sapiens
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; Publication No. US2004014239741
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT APPLICATION NUMBER: US/09/724,224
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-797-893-4
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                                                                                                                                                                                                                                                         7 PARSSAHLSQPVRVVLRVRPPLSSEAASATAPCV-SLLGCHPGGGVTVQLKD-QHTSRSE
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                                                                                           17; Length 589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                      Indels
                                                                                     33.6%; Score 593.5; DB 17; 39.2%; Pred. No. 3.2e-50; iive 71; Mismatches 107;
OTHER INFORMATION: Clone ID: MRT4577_55097C.1.pep
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                                                                                                                     Best Local Similarity 39.28
Matches 135; Conservative
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US-10-108-260A-2692
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             ; OTHER INFORMATION
US-10-425-115-320209
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US-10-108-260A-2692
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                                                                                               APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 159031

LENGTH: 377
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: AND APPLICANT: APPLICANTON: Plants FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 32209
LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 241
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33.8%; Score 597.5; DB 16; Length
Best Local Similarity 39.7%; Pred. No. 6.5e-51;
Matches 138; Conservative 69; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58448C.1.pep
US-10-437-963-159031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(377)
OTHER INFORMATION: unsure at all Xaa locations
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             Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
                                          Cao, Yor
Wu, Wei
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
           Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 OPGVIPRALMDILQLTREEGAEGRPWALSVTMSYLEIYOEKVLDLLDPASGDLVIREDCR 178
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         and Other Molecules
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38.2%; Pred. No. 1.3e-45;
tive 68; Mismatches 128; Indels
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US-10-437-963-103943
                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: LIB3689-256-H1_FLI.pep
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Best Local Similarity 37.5%; Pred. No. 2.3e-44;
Matches 126; Conservative 68; Mismatches 128;
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants and Uses Thereof FILE REPERENCE: 38-21 (53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NOS: 73128 LENGTH: 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 103943, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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PPPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Matches 132; Conservative
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ORGANISM: Oryza sativa
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ORGANISM: Zea mays
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Annua
APPLICANT: Annua
APPLICANT: Cao, Yinhua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(33.22) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 3132919
LENGTH: 783
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                         ODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 344
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICAT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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ORGANISM: Zea mays
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APPLICANT:
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RESULT 15
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                                                                                                                                                                        264 PPDTTTQAEVYSTTTSDLVEGVLQGRNGTVFCYGATGAGKTYTMLGTWESPGVWVLAIKD 323
                                                                                                                                                                                                                                                            LLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK 189
                                                                                                                                                                                                                                                                                                      PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRB-RLAPFRQREGKLYL 248
                                      :|: | ||||| : | |||| sriwsrkendagsrscvkivnkkdvyltefassetdylrlkryrgrhfcfdss 263
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APPLICANT: Yu, Ming
APPLICANT: Yu, Ming
APPLICANT: Stowner, Roman
APPLICANT: Batel, Umesh A.
APPLICANT: Davies, Katherine A.
TILE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 02052-00141008;
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
FRIOR PELING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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ARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK-
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Patent No. US20020110883A1
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 RPPPARVRVAVRLRPFV-----
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LENGTH: 383
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US-09-883-096-5
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233 RERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQG 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sakowicz, Roman
APPLICANT: Bakowicz, Roman
APPLICANT: Patel, Umesh A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 020522-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
LENGTH: 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Amino acid sequence encoded by human kinesin motor OTHER INFORMATION: proctein gene Hakip3a (Figure 1).
OTHER INFORMATION: Description of Artificial Sequence:Amino acid OTHER INFORMATION: sequence of HsKip3a.
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                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09883096
; Patent No. US20020110883A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beraud, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.77
Matches 138; Conservative
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Yu, Ming
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US-09-883-096-2
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296 TTLGLVISALADQSAGKNKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDET 355
                                                                    52 IANWRNHQETLKYQFDAFYGERSTQQDIYAGS-----VQPILRHLLEGQNASVLAYGP 104
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         11 LGGCRMG------DSKVKVAVRIRP-MNRRETDLHTKCVVDVDANKVILNPVNTNLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              223 HAVLLVKVDQRERLAPFR-----QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL
                                                                                                                                                                                        TGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLL
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APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Steart
APPLICANT: LINCOLN, Steart
APPLICANT: LINCOLN, Steart
APPLICANT: LINCOLN, Steart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113
FCT
CURRENT APPLICATION NUMBER: US/10/20,120
CURRENT FILING DATE: 2002-08-26
FO/184,769; 60/184,771; 60/184,771; 60/184,775; 60/184,776;
60/184,769; 60/184,772; 60/184,771; 60/184,811; 60/184,772; 60/184,772; 60/184,772; 60/184,772; 60/184,772; 60/184,772; 60/204,812; 60/204,981; 60/204,982; 60/205,287; 60/205,287; 60/205,285; 60/205,285; 60/205,285; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 
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; OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:403409.1.orf3:2000MAY19
US-10-220-120-366
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29.8%; Score 527; DB 15; Length 757;
Best Local Similarity 36.0%; Pred. No. 2.2e-43;
Matches 135; Conservative 69; Mismatches 127; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIU, Tommy F. ROSEBERRY, Ann M. ROSEBERRY, Bruce H. RUSSO, Frank D. STOCKDREHER, Theresa K.
Sequence 366, Application US/10220120
Publication No. US20040048253A1
                                                                                                                                                                                                                                                                                                                                                                AMSHEY, Stefan
DAHL, Christopher R.
DAM, Tam C.
DANIELS, Susan E.
DUFOUR, Gerard E.
                                                                                                                    PANZER, SCOCT R.
SPIRO, Peter A.
BANVILLE, Steven C.
SHAH, Purvi
CHALUP, Michael S.
CHANG, Simon C.
                                                                                          APPLICANT: INCYTE GENOMICS, INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FONG, Willy T. GREENAWALT, Lila B
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WRIGHT, Rachel J.
YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
                                US20040048253A1
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                                                                                                                                                                                                                                                                                                             HEN, Alice
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ORGANISM: Homo sapiens
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LENGTH: 757
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1 MGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMD-

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Sequence Sequence

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TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP
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US-09-724-224-6
i Sequence 6, Application US/09724224
j Sequence 6, Application US/09724224
j Sequence 6, Application US/09724224
j REMEMAL INFORMATION:
j APPLICANT: Beraud. Christophe
j TITLE OF INVENTION: their use
j TITLE OF INVENTION: their use
j CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
j PRIOR APPLICATION NUMBER: 09/597,292
REAUR FILING DATE: 2000-66-20
j REAURER FILING DATE: 2000-66-20
j REAURER FILING DATE: 2000-06-20
j SOFTWARE: FastSEQ for Windows Version 4.0
j SEQ ID NO 6
j LENGTH: 346
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US-09-724-517-2
US-09-641-807A-2
US-09-724-517-4
US-09-724-517-4
US-09-641-807A-4
US-09-641-806-2
US-09-641-806-2
US-09-723-129-2
US-09-723-129-4
US-09-723-129-4
US-09-723-129-4
US-09-723-129-4
US-09-723-820-8
US-09-723-820-8
US-09-723-820-8
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US-09-723-820-8
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US-09-723-820-8
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US-09-555-6848-39
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   11279
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CRGANISM: Human
US-09-724-224-6
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Best Local Simi
Matches 346;
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-724-217-4
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; TYPE: PRT
; ORGANISM: Human
US-09-724-224-8
                                                                                                                                  TYPE: PRT
CRGANISM: Human
US-10-093-317-6
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Score 1768; DB 3; Length 487; Pred. No. 2.1e-180;

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15 Sequence 8, Application US/10093317

15 Sequence 8, Application US/10093317

15 Patent No. 6762043

15 GENERAL INFORMATION:

15 APPLICANT: Beraud, Christophe

17 TILE OF INVENTION: No. 6762043el motor proteins and methods for

17 TILE OF INVENTION: their use

17 TILE OF INVENTION: their use

17 TILE OF INVENTION: their use

18 FILE REFERENCE: 1004

19 CURRENT FILING DATE: 2002-03-06

19 PALOR PILING DATE: 2002-013-06

19 PALOR PILING DATE: 2000-11-28

10 NUMBER OF SEQ ID NOS: 8

10 SOFTWARE: FastSEQ for Windows Version 4.0
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CRGANISM: Human
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Sequence 4. Application US/09724224

Setent No. 6387644

GENERAL INFORMATION:

ITILE OF INVENTION: No. 63876441 motor proteins and methods for TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/09/724,224

CURRENT FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FSELSEQ for Windows Version 4.0
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ORGANISM: Human
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                                                                                                                           ; Sequence 2, Application US/09724224
; Batent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REPERBUCE: 104
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT PILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 2, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1047
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR PILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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326 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
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Best Local Similarity 100.0%; Pred. No. 4.5e-180;
Matches 345; Conservative 0; Mismatches 0;
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LENGTH: 370
TYPE: PRT
ORGANISM: Human
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US-09-724-224-2
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TYPE: PRT
                       301
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US-09-724-511-4
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267 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 326
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                                                                                                                                        Sequence 4, Application US/10093317

Sequence 4, Application US/10093317

Sequence 4, Application US/10093317

GENERAL INFORMATION:

TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

FILE REFERENCE: 1040.093,317

CURRENT FILING DATE: 2002-03-06

PRIOR APPLICATION NUMBER: 09/724,224

PRIOR PAPLICATION NUMBER: 09/724,224

PRIOR PAPLING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 4

LENGTH: 512
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; Patent No. 6544766
; GENERAL INFORMATION:
    APPLICANT: Beraud, Cara
    APPLICANT: Sakowicz, Roman
    APPLICANT: Wood, Kenneth
    APPLICANT: Yu, Ming
    TITLE OF INVENTION: Human kinesins and methods of producing
    TITLE OF INVENTION: and purifying human kinesins
    FILE REFERENCE: cytop036
    CURRENT APPLICATION NUMBER: US/09/595,684B
                                                                                                                                                                                                                                                                                                                                                                                                                             99.7%; Score 1763; DB 4; Length 512; ilarity 100.0%; Pred. No. 7.6e-180; Conservative 0; Mismatches 0; Indels
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                                                             Similarity
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ORGANISM: Human
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US-09-595-684B-35
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Best Local Simi
Matches 345;
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60 ETLKYOFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ 119
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'Sequence 4, Application US/09724511
'Sequence 4, Application US/09724511
'Sequence 4, Application US/09724511
'General No. 63916011
'APPLICANT: Beraud, Christophe
'APPLICANT: Freedman, Richard
'APPLICANT: Freedman, Richard
'TILE OF INVENTION: their use
'TILE OF INVENTION: their use
'TILE OF INVENTION: UNMER: US/09/724,511
'CURRENT FILING DATE: 2000-11-27
'PRIOR APPLICATION NUMBER: 09/632,344
'PRIOR APPLICATION NUMBER: 09/632,344
'SPRIOR PRIOR DATE: 2000-08-03
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31.1%; Score 549; DB 3; Length 355;
Best Local Similarity 39.0%; Pred. No. 4.6e-50;
Matches 141; Conservative 59; Mismatches 114; Indels
                                                                                                                                                                                                                                        Length 665;
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; Pred. No. 1.2e-179;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 665
                                                                                                                                                                                                                                               99.7%;
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Best Local Similarity
Matches 345; Conserv
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ORGANISM: Human
                                                                                                                                                               TYPE: PRT
ORGANISM: Human
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60 ETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 VRVAVRLRP------FVDGTAGASDP-----PCVRGMDSCSLEIANWRNHQ 59
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                                                                                                                                                                                                                                                                    APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6534309el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1046
CURRENT APPLICATION NUMBER: US/09/632,344
CURRENT APPLICATION NUMBER: 2000-08-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6391601

GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REPERENCE: 1046
CURRENT PILING DATE: 2000-11-27

CURRENT PLILING DATE: 2000-08-03
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39.0%; Pred. No. 4.6e-50;
.ive 59; Mismatches 114; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                  ; Sequence 4, Application US/09632344
; Patent No. 6534309
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Best Local Similarity
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DI 354
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APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6492151e1 motor proteins and methods for
TITLE OF INVENTION: their use
FILE REPERENCE: 1046
CURRENT APPLICATION NUMBER: US/09/723,097
PRIOR APPLICATION NUMBER: 09/632,344
PRIOR APPLICATION NUMBER: 09/632,344
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Windows Version 4.0
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Patent No. 6492151
GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 355
TYPE: PRT
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US-09-723-097-4
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US-09-632-344-2
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                                                                                         Length 367;
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39.0%; Pred. No. 4.9e-50;
ive 59; Mismatches 114;
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Patent No. 6492151;
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: No. 6492151e1 motor proti
FILE REFERENCE: 1046
CURRENT APPLICATION NUMBER: 09/632,344
PRIOR FILING DATE: 2000-10-27;
RIOR PADLICATION NUMBER: 09/632,344
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity 39.0
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US-09-723-097-2
                                        ; TYPE: PRT
; ORGANISM: Human
US-09-724-511-2
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             SEQ ID NO 2
LENGTH: 367
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238 PFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL-----
                                                    180 NILIPGLS-QKPISSFADFERHFLP-ASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLA
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US-09-632-344-2
Sequence 2. Application US/09632344
Sequence 2. Application US/09632344
Sequence 2. Application US/09632344
Sequence 2. Applicant No. 6534309
GENERAL INFORMATION:
APPLICANT: Bereadad, Christophe
APPLICANT: Freedand, No. 6534309el motor proteins and methods for TITLE OF INVENTION: their use
FILE REPERENCE: 1046
CURRENT APPLICATION NUMBER: US/09/632,344
CURRENT FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4
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Search completed: November 5, 2004, 18:46:46 Job time : 14.5172 secs

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Sequence 8, Application US/09724224;
Senerat No. 6387644;
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe;
TITLE OF INVENTION: No. 6387644el motor proteins and methods for TITLE OF INVENTION: their use;
FILE REFERENCE: 1044;
CURRENT APPLICATION NUMBER: US/09/724,224;
CURRENT FILING DATE: 2000-06-20;
PRIOR APPLICATION NUMBER: 09/597,292;
PRIOR APPLICATION NUMBER: 09/597,292;
PRIOR FILING DATE: 2000-06-20;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-592-037-6
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US-09-428-1568-2
US-09-428-1568-2
US-09-428-1568-2
US-09-595-6848-29
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                                   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-724-224-6
US-09-592-054-4
US-09-592-054-6
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US-09-592-054-6
US-09-723-2191-2
US-09-723-2191-2
US-09-723-2192-2
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Battent No. 6762043
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6762043el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REPERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/093,317
CURRENT FILING DATE: 2002-03-06
PRIOR PILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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; Pred. No. 1.1e-225;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity 100.0%;
Matches 487; Conservative 0;
                                                                                       ENHCPIM 487
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Best Local Similarity
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Best Local Similarity 100.0%; Pred. No. 3.7e-225;
Matches 486; Conservative 0; Mismatches 0;
Sequence 4, Application US/09724224;
Patent No. 6387644;
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6387644el motor prot:
TITLE OF INVENTION: their use
FILE REFREENCE: 1044;
CURRENT APPLICATION NUMBER: US/09/724,224;
CURRENT FILING DATE: 2000-11-28;
PRIOR APPLICATION NUMBER: 09/597,292;
PRIOR FILING DATE: 2000-06-20;
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-093-317-4
US-10-093-317-4
; Sequence 4, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor prot
; TITLE OF INVENTION: their use
; CURRENT APPLICATION NUMBER: US/10/093,317
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100.0%; Pred. No. 5.6e-225;
ive 0; Mismatches 0;
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Sequence 6, Application US/09724224

Patent No. 6387644

GENERAL INFORMATION:
TITLE OF INVENTION: No. 6387644el motor prot.
TITLE OF INVENTION: No. 6387644el motor prot.
TITLE OF INVENTION: their use
FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/09/724,224

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FRSESEQ FOR WINGOWS VERSION 4.0
                                                                                                                                al Similarity 100.
486; Conservative
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NHCPTM 511
             ; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-35
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; TYPE: PRT
; ORGANISM: Human
US-09-724-224-6
        LENGTH: 665
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Best Local S
Matches 486
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Fatent No. 6544766
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: cytop036
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: cytop036
CURRENT APPLICATION NUMBER: 09/295,612
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR PILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                    Length 512;
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99.8%; Score 2467; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.7e-225;
Matches 486; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/724,224
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Human
US-10-093-317-4
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LENGTH: 370
TYPE: PRT
ORGANISM: Human
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US-09-724-224-2
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US-10-093-317-2
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1 MGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQE 60
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                                                                                       61 TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP
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## SERRATION SECTION OF TITLE OF INVENTION: THE OF INVENTION OF THE CONTROL OF THE C
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100.0%; Pred. No. 4e-159;
tive 0; Mismatches C
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Best Local Similarity 100.
Matches 346; Conservative
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US-10-093-317-6
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US-10-093-317-6
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                                               GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor proteins and methods for
TITLE OF INVENTION: Lheir use
FILE REFERENCE: 104
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
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100.0%; Pred. No. 1.3e-158;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
Sequence 2, Application US/09724224
Patent No. 6387644
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Best Local Similarity
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us-10-797-893-8.rai

Qy 299 SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNPAARSKEVINRPFTNESLQPHA 358	TITLE OF INVENTION: No. 6440684el motor proteins and methods for intial or INVENTION: their use FILE REPERENCE: 1016 CURRENT APPLICATION NUMBER: US/09/592,054 CURRENT FILING DATE: 2000-07-20 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 TYPE: PRT ORGANISM: Human US-09-592-054-4 Query Match Best Local Similarity 31.8%; Score 572; DB 4; Length 522; Best Local Similarity 31.8%; Pred. No. 2.1e-45; Matches 165; Conservative 99; Mismatches 167; Indels 88; Gaps 17; OY I MGRCRLSKIGATRRPPARVRVAVRLRP	99 VLAYGTDKSPTYDFVFDPSTEQEEVENTAVAPLIKGVFKGYNAT 99 VLAYGGTGSGKTYSMGGAYTAEQENEPTVGVIPRALMDLQLTREEGAEGRPWALSVTMS 104 VLAYGGTGSGKTYSMGGAYTAEQENEPTVGVIPRVIQLLFKEIDKKSDFETLKVS 1104 VLAYGGTGSGKTYSMGGAYTAEQENEPTVGVIPRVIQLLFKEIDKKSDFETLKVS 1105 YLEIYOEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRT 1100 VLAYGGTGSGKTYSMGGAYTAEQENEPTVGVIPRVIQLLFKEIDKKSDFETLKVS 110 VGATRLNORSSRSHAVLLVVVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNGGLRLKE 110 VGATRLNORSSRSHAVLLVVVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNGGLRLKE 111
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; CarcalskidatrapparvavavalarspychoctagasDppcvRcmoscSleIanwrN40eT 0	RESULT 10 US-09-592-054-8 US-09-592-054-8 Sequence 8, Application US/09592054 Sequence 8, Application US/09592054 Sequence 8, Application US/09592054 Setent No. 6440684 GENERAL INFORMATION: APPLICANT: Beraud, Christophe APPLICANT: Sakowicz, Roman APPLICANT: Wood, Kenneth APPLICANT: Wood, Kenneth TITLE OF INVENTION: No. 6440684el motor proteins and methods for TITLE OF INVENTION: Lheir use FILE REFERENCE: 1016 CURRENT APPLICATION NUMBER: US/09/592,054 CURRENT APPLICATION NUMBER: US/09/592,054 CURRENT PILING DATE: 2000-07-20 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NOS: 8 LENGTH: 1234 TYPE: PRT TYPE: PRT TYPE: PRT OP-592-054-8	Query Match 23.2%; Score 573.5; DB 4; Length 1234; Best Local Similarity 32.2%; Pred. No. 6.1e-45; Added: Sp. Gaps 13; Matches 156; Conservative 97; Mismatches 173; Indels 59; Gaps 13; Qy 20 VRVANELRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAF 69 :

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-----TLPGSITVEPSENLQSLMEKNQSLVEENEKLSRGLSEAAGQTAQML----ER 439
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GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: Lebir use
FILE REFERENCE: 1016
CURRENT PAPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
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                           445 MVLMKTVEEK-DLEIERLKTKOK-ELEAKMLAOKAEEKE
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Patent No. 6440684
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32.3%;
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                                                                                              RESULT 12
US-09-592-054-6
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SEQ ID NO 6
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Best Local &
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RESULT 13 US-09-592-054-2 ; Sequence 2, Application US/09592054

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
GENERAL INFORMATION:
APPLICANT: Beraud, Jeffrey
APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOCTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1232
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Sequence 2, Application US/09572191

Sequence 2, Application US/09572191

Sequence 2, Application US/09572191

Sequence 2, Application Gassafe

Paranta INFORMATION:

APPLICANT: Baraud, Christophe

APPLICANT: Sakowicz, Roman

APPLICANT: Wowler: Application No. 6355466el motor proteins and methods for TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

FILE REFERENCE: 1017

CURRENT APPLICATION UNMBER: US/09/572,191

CURRENT PILING DATE: 2000-05-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.7%; Score 561.5; DB 4; Length 1232; 32.0%; Pred. No. 8.3e-44; ive 97; Mismatches 163; Indels 75;
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Best Local Similarity 32.0%
Matches 158; Conservative
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US-09-592-054-2
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246
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Fatent No. 6379912
GENERAL INFORMATION:
APPLICANT: Baraud, Christophe
APPLICANT: Baraud, Christophe
TITLE OF INVENTION: No. 6379912e1 motor proti
TITLE OF INVENTION: their use
FILE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/723,262
CURRENT FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1388
                                                                                                                               22.7%;
                                                                                                                             Query Match
Best Local Similarity 30.9*
Matches 162; Conservative
                                                               ; TYPE: PRT
; ORGANISM: Human
US-09-572-191-2
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22.7%; Score 561; DB 3; Length 1388;

Query Match

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                   74; Gaps
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al Similarity 30.9%; Pred. No. 1.1e-43; 162; Conservative 97; Mismatches 192; Indels
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Best Local Similarity
Matches 162; Conserv
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November 5, 2004, 18:44:52; Search time 82.6338 Seconds (without alignments) 2081.726 Million cell updates/sec
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2472
1 MGRCRLSKIGATRRPPPARV.....LEAKWLAQKAEEKENHCPTM 487
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		-4 Sequence 4, Appli		S		-2 Sequence 2, Appli						-8 Sequence 8, Appli	
	ID	US-10-797-893-8	US-10-797-893	US-10-334-143	US-09-925-300-1	US-10-797-893	US-10-797-893	US-10-425-115	US-10-437-963	US-10-334-143	US-10-116-712	US-10-408-765	US-10-334-143-8	US-10-437-963-
	DB	16	16	15	6	16	16	17	16	15	14	16	15	16
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	Query	100.0	8.66	93.4	9.98	71.5	71.3	24.6	24.3	23.4	23.2	23.2	23.5	23.1
	Score	2472	2467	2309	2141	1768	1763	608	601	578.5	574.5	574.5	574.5	571
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Sequence 332919, Sequence 59708, A Sequence 2692, Ap Sequence 231231, Sequence 82, Appl Sequence 32, Appl		Sequence 669, App Sequence 669, App Sequence 314, App Sequence 366, App Sequence 316, App Sequence 2, Appli	Sequence 1, Appli Sequence 1477, Ap Sequence 306, App Sequence 25, Appl Sequence 114, Appl Sequence 6, Appli	Sequence 13, Appl Sequence 112, App Sequence 176714, Sequence 6, Appli Sequence 2, Appli Sequence 472, App
US-10 US-10 US-10 US-10 US-10	US-10-332-089-2 US-10-188-832-16 US-10-290-79 US-10-287-226-14 US-10-425-114-62	- SU - SU - SU - SU - SU - SU	US-10-458-162-1 US-10-408-765A-1 US-10-287-226-30 US-10-080-608A-21 US-10-332-089-6	US-10-080-608A-23 US-10-370-685-112 US-10-437-963-176714 US-10-601-036-6 US-10-601-036-2 US-10-282-174-472
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 487;
Sequence 8, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: 000461
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR PILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 487; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 487
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267 RECKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 326
                                                                                                                                                                                                                                                                                        Sequence 80, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR VACHESLAVOVICH
APPLICANT: GUDARGANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REWOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: METHOD FOR DETECTING REWOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: MARSHER 105/10/334,143
CURRENT APPLICATION NUMBER: 05/212-31
PRIOR APPLICATION NUMBER: 05/343,169
PRIOR FILING DATE: 2001-12-31
NUMBER 05 SEQ ID NOS: 207
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                                          VYLISQKELLIGPPEAKRARGPEEERIGSPEPMAAPASASQKLSPLQKLISSMDPAMLERLLIS
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                              TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
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US-10-334-143-80
                                                                                                                                                                                                     NHCPTM 487
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US-10-334-143-80
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LENGTH: 490
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TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/99/724,224
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.8%; Score 2467; DB 16; Best Local Similarity 100.0%; Pred. No. 2.7e-201; Matches 486; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10797893
Publication No. US20040142397A1
GENERAL INFORMATION:
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US-10-797-893-4
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                                                                               Sequence 6, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFREEME: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT PILING DATE: 2004-03-09
; PRIOR PILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 346
; TVPE: DATE: 200
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Sequence 2, Application US/10797893

Publication No. USZ0040142397A1

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: Novel motor proteins and methods for

TITLE OF INVENTION: Heir use

FILE REFERENCE: 1044

CURRENT FILING DATE: 2004-03-09

PRIOR PPLICATION NUMBER: US/09/724,224

PRIOR PLILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

SROID NOS: 8

SOFTWARE PESTSRO for Windows Version 4.0

SEQ ID NO: 1370
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100.0%; Pred. No. 5.8e-142;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 346; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Human
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LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1228
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                                                                                                                                                Sequence 1228, Application US/09925300
| Patent No. US20020151681A1
| GENERAL INFORMATION:
| APPLICANT: Craig Rosen,
| APPLICANT: Steve Ruben,
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies,
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies,
| FILE REFERENCE: PA101
| CURRENT APPLICATION NUMBER: US/09/925,300
| PRIOR APPLICATION NUMBER: PCT/US00/05988
| PRIOR APPLICATION NUMBER: 60/124,270
| PRIOR APPLICATION NUMBER: 60/124,270
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1890
| SEQ ID NOS: 1890
| SEQ ID NO 1228
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                              454 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDL 488
422 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                  US-09-925-300-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 460
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Sequence 159031, Application US/10437963
; Sequence 159031, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: A Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Burbazuk, Brad
; APPLICANT: Burbazuk, Brad
; APPLICANT: Burbazuk, Brice Nucleic Acid Molecules and Other Molecules Associated With
; APPLICANT: Burbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KELLGP----PEAKRARGPEEEEIGSPEPMAAP-----ASASOKLSPLOKLS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 KIKKILFDPVVHVPTENIPKEHRQTEVNTPKKVVLPSVTPCNEKHEASLRKALSPIS--S 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMDPAMLERLLSLDRLLASQGSQGAPLL---STPKRERMVLMKTVEEKDLE-IERLKTKQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 NMVP------VEQQIPDNGN--CPVLLEPQTPIEKRNIVEETPGATPLERFNALGSNL 515
                                                                                                                                                                                                                                                         RILODSIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFINESLOP----- 356
                                                                                                                                                                                                                                                                                                       DMEAKLRAWLESKGKTKSIQRMDGLFSPIASKTPLSVSHMKQPTSSRIPCRVKAMDQDGG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
EGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_58448C.1.pep
US-10-437-963-159031
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 KEALVQQYLDLLNVANKEE 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 36.7%
Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
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Publication No. US20040214272A1
GENERAL INFORMATION:
CENTRAL INFORMATION:
CONTREMY:
COURRENT PERFERENCE:
CURRENT FILING DATE:
CURRENT FI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205
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24.6%; Score 608; DB 17; Length 589;
Best Local Similarity 31.1%; Pred. No. 1e-42;
Matches 174; Conservative 94; Mismatches 163; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQGET
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                                                                                                                                                                                Length 370;
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US-10-425-115-320209
                                                                                                                                                                                Query Match 71.3%; Score 1763; E
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 345; Conservative 0; Mismatches
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                                                                            , ORGANISM: H1
US-10-797-893-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIRE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAPPROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPR-- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 LQPHALGPVK--LSQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSP-LQKLSS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 POTAELNHLKOOVOOLOVL----LLOAHGG-----TLPGSITVEPSENLOSLME 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 MDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-EL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 PTVGVIPR----VIQLLFKEIDKKSDFEFTLKVSYLEIYNEEILDLLCPSREKAQINIRE
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     119 LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-ELEAKMLAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VRVAVRLRP------FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
                                                                                                                                                                                                                                                                                     APPLICANT: Switzer, Ann
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILLE PERENEWE: 210121.568
CURRENT APPLICATION NUMBER: US/10/116,712
CURRENT FILLING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 670
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.2%; Score 574.5; DB 14; Length
32.5%; Pred. No. 2.2e-39;
ive 97; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-10-408-765A-2153
; Sequence 2153, Application US/10408765A
                                                                                                                                                                                                            ; Sequence 670, Application US/10116712; Publication No. US20030194764A1; GENERAL INFORMATION: APPLICANT: Bangur, Chaitanya S.
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DLQKLVETLEDQE 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 32.59
Matches 160, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                      |::|
LEDQE 461
                                                                              477 AEEKE 481
                                                                                                                                                                         RESULT 10
US-10-116-712-670
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                                                                                                                                   221 VKGKLNLITSXDLAGNEDNRRTCNEGIRLQESAKINQSLFALSNVISALNKKEPRIPYRE 280
                                                                                                                                                                                                            281 SKLTRILQDSLGGNSHAVMIACLNPVE--YQEAVHTVSLAARSRHVTN------HM 328
LMXSTVLALCTGT------WC-SVEISYYEVYMERCYDLLEPKAREIMVLDDKDGNL 167
                                                                                                                                                                                        SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIREDCRGN 180
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                                                              LIPGLSQKPISSPADPERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                            242 REGKLYLI----DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRD
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APPLICANT: GRIGORLEY, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOWOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REPERENCE: 038602/1543
CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR PILING DATE: 2001-12-31
NUMBER: OF SEQ ID NOS: 207
SOFTWARE: PALCHIN Ver. 2.1
                                                                                                                                                                                                                                                                 359 LGPVKLSQKELLGPPEAK-----RARGPEE-----EEIGSPEPMAAPASASQ 400
                                                                                                                                                                                                                                                                                       329 SSASKXKDKVDM---BAKLRAWLESKGKTKSIQRMDGLLSPNAIKTPLSMSQ 377
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Pred. No. 1e-39;
7; Mismatches 172; Indels 59;
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Publication No. US20040009549A1
GENERAL INFORMATION:
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Best Local Similarity 32.4*
Matches 157; Conservative
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354 LQPHALGPVK--LSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSP-LQKLSS 410
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Sequence 8, Application US/20040009549A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GRIGORLEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REPERENCE: 038602/1543
                                                                               APPLICANT: Zhang, Bing
APPLICANT: Shang, Bing
APPLICANT: Glean, Bradford W.
APPLICANT: Glean, Gary M.
APPLICANT: Glean, Gary M.
APPLICANT: Glean, Gary M.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 10 DENTIFIED IN THE MITOCHONDRIAL PROTEOME
CURRENT APPLICATION UNDER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
23.2%; Score 574.5; DB 16; Length 1232;
Best Local Similarity 32.5%; Pred. No. 2.2e-39;
Matches 160; Conservative 97; Mismatches 161; Indels 75;
Publication No. US20040101874A1
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DLOKLVETLEDQE 458
                    GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-408-765A-2153
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US-10-437-963-103943

Sequence 103943, Application US/10437963

Sequence 103943, Application US/10437963

Sequence 103943, Application US/10437963

Sequence 103943, Application US/10437963

Sequence 103943, Application US/10437,963

Sequence 103943, Application US/10437,963

Sequence 103943

Sequence 103943, Application US/10437,963

Sequence 103943, Application US/10437,963

Sequence 103943

Sequence 103943
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                                                                                                                                                                                                                                                                                               20 VRVAVRLRP------PVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY
                                                                                                                                                                                                                         Query Match
23.2%; Score 574.5; DB 15; Length 1235;
Best Local Similarity 32.5%; Pred. No. 2.2e-39;
Matches 160; Conservative 97; Mismatches 161; Indels 75;
                                                                                                                                                                                                                                                                                                                                  13 VRVALRCRPLVPKEISEGCQMCLSFVPG----EPQVVVGTDK----
CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/343,169
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1235
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449 DLQKLVETLEDQE 461
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US-10-334-143-8
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Best Local S
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squence 59708, Application US/10425114

publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REPERENCE: 38-21 (5313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SSQ ID NO 59708
LENGTH: 854
                                                                                                                                                                                                                       119 OPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 NPGVMVLAINDLFSKVTQKNH-----SIKLSYLEIYNETVRDLLSPGS-PLNLREDKQ 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 -QPHALGPVKLS-QKE--LLGPPEAKRARGPEEEFIGSPEPMAAPASASQKLSPLQKLSS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         603 STPGSTQRKTRRSILAAGGGNYFSKLDSKRHAADNAQVRELQRKVSTLESEIEKWK-KEH 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 KIGA-TRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK---
                                                                                                                                                                                                                                                                                                         ----YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 FROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRD
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                                                                  Length 783;
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33.6%; Pred. No. 2.5e-39;
.ive 91; Mismatches 195; Indels
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US-10-425-114-59708
                                                            23.1%; Score 571; DB 17; ilarity 33.6%; Pred. No. 2.2e-39; Conservative 91; Mismatches 195;
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Best Local Similarity 33.6%
Matches 163; Conservative
                                                                                           Similarity
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US-10-425-115-332919
                                                                                                                        Matches 163;
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Publication No. US20040214272A1
Publication No. US20040214272A1
REBERGIONE INFORMATION:
APPLICANT: Ex Rosa, Thomas J.
APPLICANT: Exou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: 105/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 332919
LENGTH: 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 RAYSTDEVMKLLQQGNQNRTTEPTRVNETSSRSHAILQVIVEYRSIDGGSIVTRVGKLSL 438
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                                                                                                                                                                                                                                                                                                                                                                        264 PPDTTTQAEVYSTTTSDLVEGVLQGRNGTVPCYGATGAGKTYTMLGTMESPGVMVLAIKD
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                                                                                                                                                                                                             Length 776;
                                                                                                                                                                                                    h 23.1%; Score 571; DB 16; Length 7 Similarity 31.5%; Pred. No. 2.2e-39; 52; Conservative 99; Mismatches 194; Indels
                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_101324C.1.pep
US-10-437-963-103943
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OTHER INFORMATION: unsure at all Xaa locations FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_66737C.1.pep
                      TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Zea mays
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Best Local Sim:
Matches 152;
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                                                                                                                     388 NPGVWVLAINDLFSKVTQKNH-----SIKLSYLEIYNETVRDLLSPGS-PLNLREDKQ 439
                                                                                                                                                                                                                                        355 -QPHALGPVKLS-QKE--LLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSS 410
                                                                                                                                                                                                                                                                                                                                                                                                                268 EVGAGTAEAAESRILVFVRLRPMSRKEKEAGSRSCVKIVNRKEVFLTESASENDYLRLKR 327
                                       64 ----YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPE 118
                                                                                                    119 OPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYOEKVLDLLDPASGDLVIREDCR 178
                                                                                                                                                             179 GNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQRERLAP 238
                                                                                                                                                                           239 FROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRD 298
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5, 2004, 19:09:49 Search completed: November Job time : 83.6338 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 5, 2004, 18:34:12; Search time 14.1983 Seconds
(without alignments)
3300.235 Million cell updates/sec

Title:

US-10-797-893-8

Perfect score: 2472
Sequence:
1 MGRCRLSKIGATRRPPPARV......LEAKMLAQKAEEKENHCPTM 487

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283416 seqg, 96216763 residues
```

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

283416

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAA----------PASASQ 400

361

8 8 8

kinesin-related pr	kinesin-like spind	kinesin heavy chai	kinesin-related pr	kinesin-like prote	kinesin-related pr	kinesin heavy chai	kinesin-like prote	kinesin heavy chai	hypothetical prote	kinesin-related pr	kinesin-like prote	centromere protein	kinesin-like prote	kinesin heavy chai	hypothetical prote
S58691	G02157	S44868	A40264	A55289	S64238	A38713	833417	A35075	T20621	JN0114	T15822	S28261	T46242	837711	T06065
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742	1056	843	1060	1150	805	1031	1067	196	958	1584	1584	2663	813	1027	1121
21.6	21.5	21.4	21.3	21.2	21.1	21.1	21.1	21.0	21.0	21.0	21.0	20.9	20.9	20.7	20.7
533	532	529.5	525.5	525	522.5	520.5	520.5	519	518.5	518	518	517	516	512	511
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

noue, '

RESULT 1 S62318 Kinesin-like DNA binding protein KID - human C.Species: Homo sapiens (man) C.Species: Mug-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-200 C.Speciesion: S63228 R.Tokai, N.; Fujimoco-Nishiyama, A.; Toyoshima, Y.; Yonemura, S.; Tsukita, BEBO J. 15, 457-467, 1996 A.Fitle: Kid, a movel kinesin-like DNA binding protein, is localized to chanks the serious cype: MID: 96174806; PMID: 859929 A.Accession: S6328; MUID: 96174806; PMID: 859929 A.Accession: March A.Molecule type: mRNA A.Molecule type: mRN	IIIPGLGGKPISSPADFBRHFLPASRNRTYGATRINGRSRSHAVLLVKUDGRERLAPFR 	QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNGGLFRVPYRDSK 	LTRILQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALG
SESULT 1 S62328	181	241	301
RESULT 1 S62328 kinesin- C;Speciec C;Date: 'C;Access R;Citalian A;Ritle: A;Residum A;R	o B	ζ q	රු පු

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Cyaccesion: A55256; E41298

Kipesvento, P.A.; Stewart, R.J.; Goldstein, L.S.B.
J. Cell Biol. 127; 1041-1048, 1994

A.Title: Characterization of the KLP68D kinesin-like protein in Drosophila: possible rohy Reference number: A55236; MUID:95050960; PMID:7525600

A,Reference number: A55236

A,Reference number: A55236

A,Residues: 1-784 <-PESS

A,Residues: 1-784 <-PESS

A,Residues: L-784 <-PESS

A,Reference number: A41298; MUID:92020874; PMID:1924306

A,Recession: E41298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: may be part of a motor protein that provides anterograde fast axonal 16;Description: winesin_related protein KIF3; kinesin motor domain homology C;Reywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop F;1-34)Fomain: head globular #status predicted cHGL> F;0-350/Domain: head globular #status predicted cHGL> F;00-350/Domain: head globular motor domain homology cMOT> F;00-350/Domain: winesin motor domain homology cMOT> F;80-80/Domain: helical rod #status predicted cHCL> F;81-784/Domain: tail globular #status predicted cHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 RERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | : | : | : | : | : | | 353 DPQ-----DAKLKEYQEBERLKRLIGPQQQQRSEKQYTAKKQRVKRPKKETVTKEMSDS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDCRGN-ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SRRPGTGSSQTPNECVQVVVRCRPMSNRERSERSPEVVNVYPNRGV----VELQNVVDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN
                              C;Species: Drosophila melanogaster
C;Species: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 'TC',222-337,'VRGQV' <STE>
A; Cross-references: GB:M74431; NID:g157791; PIDN:AAA28658.1; PID:g157792
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RGPEEEEI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 612; DB 1; L; Pred. No. 1.4e-33; 84; Mismatches 184;
N,Alternate names: kinesin-like protein 5; KLP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: FlyBase:Klp68D; KLP5
A;Cross-references: FlyBase:FBgn0004381
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.8%;
Best Local Similarity 33.0%;
Matches 175; Conservative 8
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                                                                                                                                                                                                                                                                kinesin-like protein - Arabidopsis thaliana
NiAlternate names: protein TIE22.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T4828
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24489
A;Reference number: Z24489
A;Reference number: Z24489
A;Reference number: Z24489
A;Residues: 1-664 <-BEV-
A;Residues: 1-664 <-BEV-
A;Residues: 1-664 <-BEV-
A;Residues: 1-664 <-BEV-
A;Reperences: UNIPROT:Q9L288; EMBL:AL162874
A;Resperimental source: cultivar Columbia; BAC clone TIE22
C;Genetics:
A;Map position: 5
A;Introns: 58/3; 128/2; 184/3; 310/1; 378/3; 480/2; 501/3; 535/1; 607/3; 628/3
A;Note: TIE22.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 ARVRVAVRLRPFV-----DGTAGASDPPCVRGMDSCSLEIANWRNHQETLK---YQFDA
           ---PGEPGAPLLSTPKRERMVLMKTVEEKDLEIER
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A55236
kinesin-related protein KLP68D - fruit fly (Drosophila melanogaster)
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32.1%; Pred. No. 8.2e-34;
tive 94; Mismatches 187;
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C;Accession: I51617; A48835; S48837
R;Vernos, I.; Raats, J.; Hirano, T.; Heasman, J.; Karsenti, E.; Wylie, C.
Call 81, 117-127, 1995
A;Title: Xklp1, a chromosomal Xenopus kinesin-like protein essential for spindle organ;
A;Reference number: A5621; MUD:95236444; PMID:7720067
A;Recence number: A5621; MUD:95236444; PMID:7720067
A;Recence number: A5621; MUD:95236444; PMID:7720067
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1226 AVENA
A;Residues: 1-1226 AVENA
A;Residues: 1-1226 AVENA
A;Residues: J.; Heasman, J.; Wylie, C.
Dev. Biol. 157, 232-239, 1993
A;Reference number: A48835; MUD:93246065; PMID:8482413
A;Recession: A48835
A;Reterence number: A48835
A;Reterence numbe
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 VRVALKCRPLVP------KENNEGCKMCLTFVPGEQQVIVGTEKSFTYDYVFDPSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETL----KYQFDAFYGERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 TQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQP--GVIPRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDLLQLTREEGAEGRP-WALSVTMSYLEIYQEKVLDLLDPA---SGDLVIREDCRGNILI
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C,Genetics:
C,Superfamily: kinesin motor domain homology
C,Keywords: ATP; nucleotide binding; P-loop
F;9-343/Domain: kinesin motor domain homology <KMOT>
F;9-34/Region: nucleotide-binding motif A (P-loop)
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23.4%; Score 579.5; DB 2;
Best Local Similarity 32.1%; Pred. No. 4.3e-31;
Matches 157; Conservative 95; Mismatches 172;
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                                                                                                             F25116.11 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86319
C;Accession: A86319
C;Accession: A86319
C;Accession: A86319
C;Arcession: A86319
C;Arcession: A86319
C;Arcession: Asidopsis H; Hulzar, L; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.;
Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C;A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Southwick, A.M.; Sun, H.; Tallon,
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Recession: A86319
A;Stetus preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-703 <STO>
A;Cross-references: UNIPROT:Q9FZ77; GB:AE005172; NID:g9795601; PIDN:AAF98419.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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kinesin-like protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.2%; Score 597.5; DB 2; 33.9%; Pred. No. 1.2e-32; ive 88; Mismatches 172;
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Matches 173; Conservative
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A;Map position: 3
A;Introns: 56/2; 99/3; 151/3; 310/3; 343/2; 395/3; 419/1; 444/3; 462/3; 489/3; 527/1; 5
A;Note: F16L2.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinesin-related protein-like - Arabidopsis thaliana kinesin-related protein-like - Arabidopsis thaliana (%)Alternate names: protein F1612.60 ($)Species: Arabidopsis thaliana (mouse-ear cress) ($)Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 ($)Accession: T47525 ($)Ascession: T47525 ($)Ascession: W; Bangert, S; Wiedelmann, R; Voss, H; Unseld, M; Mewes, H.W.; Rudd, submitted to the Protein Sequence Database, March 2000 ($)Ascession mumber: 224468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LKYQ-------FDAFYGERSTQODIYAGSVQPILRHLLEGQNASVLAYGPTGAGK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 THTMLGS------PEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVL 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQ 119
                                                                                                                                                             PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA---SGDLVIRED 176
                                                                                                                                                                                                                                                                                                                                                                                                               168 PKEGIKIVGLTERNVASARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQKKKN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 VPYRDSKLTRLLQDSLGGNSHTLMIACVSPADSNLEBTLNTLRYADRARKIKNKPIVNVD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 PQAAELNHLKQQVQQLQVLLQAHGGTLPVSINSMAPSENLQSLMEKNQSLMEENEKLSR 407
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   99
                                                              51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 RLSKIGATRRPPPAR---VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology,
                                                                                                                                                                                                                                                                                      177 CRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRINORSSRSHAVLLVKVDQRERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 LQPHALGPVK--LSQKELL-----GPPEAKRARGPEEEIGSPEPMAAPASASQKLS-
---SDPPCVRGMDSCSLEIANWRNHQETLKYQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 APFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPR---
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29.5%; Pred. No. 3.4e-30;
tive 99; Mismatches 201; Indels
                                                          PVRV---VRCRPLVPKETSEGCOMCLSFVPGEPOVIVGSDKA---
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A,Experimental source: cultivar Columbia; BAC clone F16L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLKTKOKEL----EAKMLAQKAEEKEN 482
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             PARVRVAVRLRPFV--DGTAGA---
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Best Local Similarity 29.59
Matches 156; Conservative
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A;Molecule type: DNA
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A,Residues: 1-1225 <WAN>
A,Cross-references: UNIPROT:Q90640; GB:U18309; NID:g603760; PIDN:AACS9666.1; PID:g603761
R;Wang, S.Z.; Adler, R.
Proc. Natl. Acad.
A,Title: A developmentally regulated basic-leucine zipper-like gene and its expression i
A,Reference number: A53451; MUID:94151328; PMID:8108415
      Notewaster, 1.2 McCaffrey, G.; Vale, R.D.
Submitted to the EMBL Data Library, November 1995
Submitted to the EMBL Data Library, November 1995
A; Reference number: Z18853
A; Accession: T1827
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 STQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDL--- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOLTREEGAEGRPWALSVIMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 PVSSNIRVVCRVRPLTELEKGRNEHSIVHFFDSKSISIRANGP-----QFTFDRIFGYQ 77
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J. Cell Biol. 128, 761-768, 1995
Airlus Chromokinesin: a DNA-binding, kinesin-like nuclear protein.
Aireference number: A56514; MUID:95181533; PMID:7876303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLG
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A;Molecule type: mRNA
A;Residues: 728-1086,'RI' <WA2>
A;Cross-references: EMBL:U04821; NID:g440792; PIDN:AAA18960.1; PID:g440793
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                         15 PPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEI-ANWRNHQETLKYQFDAFYGER
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                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                Length 1254;
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Best Local Similarity 31.3%; Pred. No. 3.5e-30;
Matches 159; Conservative 103; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                Query Match 22.9%; Score 567; DB 2; Length 12
Best Local Similarity 36.1%; Pred. No. 3.1e-30;
Matches 126; Conservative 79; Mismatches 132; Indels
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Accession: T18277
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ngaku, M.; Hirokawa, N. angaku, M.; Hirokawa, N. stem. stem. sg220469; PIDN:BAA02166.1; PID:g2204 sg220469; PIDN:BAA02166.1; PID:g2204 cir3A/3B heterodimer associates with crovides anterograde fast axonal tra motor domain homology ner; microtubule binding; nucleotide	RESULT 10 A57107 kineain-related protein KIF3B - mouse C;Species: Mus musculus (house mouse) C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 C;Accession: A57107 R;Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N. J. Cell Biol. 130, 1387-1399, 1995 A;Title: KIF3AB: a heterodimeric kineain superfamily protein that works as a microtubn A;Reference number: A57107; MUID:96032268; PMID:7559760 A;Recession: A57107 A;Recession: A57107 A;Residues: 1-747 < VAM>A;Residues: 1-747 < VAMAA A;Residues: 1-747
Query Match 22.8%; Score 563.5; DB 1; Length 701; Best Local Similarity 30.2%; Pred. No. 2.3e-30; Matches 169; Conservative 83; Mismatches 184; Indels 123; Gaps 16; Qy 9 IGATRRPPPA-RVRVAVRLRPF	Ouery Match 22.8%; Score 563; DB 1; Length 747; Best Local Similarity 30.7%; Pred. No. 2.8e-30; Matches 169; Conservative 95; Mismatches 189; Indels 98; Gaps 16; Qy 20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERST 75
Db 3 INKSEKPESCDNVKVVVRCRPILNEREKSMCYRQAVSVDEMRGTITVHKTDSSNEPP 58 QY 45 MDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGP 104	KEKA RHLL DSVL
OY 105 TGAGKTHTMLGSPEOPGVIPRALMDLL-OLTREEGAEGRPWALSVTMSYLEIYQEKV 160	Qy 132 QLTREEGAEGRPWALSVTWSYLEIYQEKVLDLID-PASGDLVIREDCRGNILIPGLSQKP 190

Db 234 AAAQKPGAKKDDSNHVRVGKLNLVDLAGSERQDKTGATGDRLKEGIKINLSLTALGNVIS 293 Qy 286 ALNQGLP-RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRPYLDTVSALNFAARSKEV 344	PRESULT 12 High Transin-related cytokinesis protein [imported] - Arabidopsis thaliana Cipacias: Arabidopsis thaliana (unsuchable kinesin-related cytokinesis protein [imported] - Arabidopsis thaliana (corpecies: Arabidopsis thaliana (corpecies: Arabidopsis thaliana (corpecies: Arabidopsis thaliana (corpecies: Academy 18-7); S. Faurus 40.5. Thuran, C.D.; Pujii, C.Y.; R. Cocession: H84777 M. Jarman, M.C.; Mülte, J. S. S. Stomin, L.A.; San, M.; Vandken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, M.C.; Mülte, J. S. Bean, J. A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.; Jackersen enuber: Ad420; WUID:20081487; PMID:10617197 A. Macure 40.7. Feel Minhary A. Macladues type: DNA A. Macladues 1-1056 scm. A. Macl	
Db 184 TKSVKEIEHVMAVGQNRSVGATNMNEHSSRSHAIFVITIECSEVGLDGENHIRVGKLNL 243 Qy 249 IDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOG-LPRVPYRDSKLTRLLQD 307 108 SLGGSARTGAGGERLKEATKINLSLSALGNVISALVDGKSTHIPVRDSKLTRLLQD 303 Qy 308 SLGGSARTGAGGERLKEATKINLSLSALGNVISALVDGKSTHIPVRDSKLTRLLQD 303 Qy 308 SLGGSARTGAGGERLKEATKINLSLSALGNVISALNFPTNE	46 LEAKMLAOKAE 198 46 LEAKMLAOKAE 478 514 LESKLQAVKAE 594 520.11	

RESULT 14 B84687 probable kinesin-like spindle protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004	Circlession: B8458/ Ribin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y., M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999 A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	A;Accession: B84687 A;Accession: B84687 A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Rolecule type: DNA A;Resions: 1-1076 <sto> A;Resions: 2 C;Genetics: 2 C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology</sto></sto></sto></sto></sto></sto>	Query Match 22.7%; Score 560.5; DB 2; Length 1076; Best Local Similarity 31.0%; Pred. No. 6.9e-30; Matches 159; Conservative 94; Mismatches 199; Indels 61; Gaps 14; Qy 20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQEDAFYGERSTQ 76 ::	F-F 0	170 QIFDILEAQSAAEYSLKVSFLELYNEELTDLLAPEETKFADDKSKKPLALMEDGKG 180 NILIPGLSQKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF 226 GVFVRGLEEEIVSTADEIYKVLEKGSAKRRTAETLLNKQSSRSHSIFSVTHIKECTPEG	Qy 240 RQREGKLYLIDIAGSEDNRRTGKGLRLKESGAINTSLFYLGKVVDALNQGLPRVPYR 297 :	Qy 358 ALGPVKLSQXELLGPPEAKRARGPEEEIGSPEPMAAPASASQXLSPLQKLSSMDPA 414	Qy 457 EIERLKTKOKELEAKMLAQKAEEKEN 482	C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: D86151 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
QY 347 RPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAFASASQKLSPLQ 406 362 KPEVNQKMMKSTLIKDLYGE	460 RLKTKQKELEAKWLAQKAE 478 1 : :	RESULT 13 T02017 kinesin-related protein TKRP125 - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 26-Peb-1999 #sequence_revision 26-Peb-1999 #text_change 09-Jul-2004 C;Accession: T02017 R;Asada, T.; Kuriyama, R.; Shibaoka, H. J. Cell Sci. 110, 179-189, 1997 A;Title: TKRP125, a kinesin-related protein involved in the centrosome-independent organ	A;ACCESSION: T02017 A;ACCESSION: T02018 A;ACCE	F;10-361/Domain: kinesin motor fondin homology <rmot> Query Match 22.7%; Score 560.5; DB 2; Length 1006; Best Local Similarity 30.1%; Pred. No. 6.38-30; Matches 153; Conservative 98; Mismatches 196; Indels 61; Gaps 12;</rmot>	VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERS 74	67 123 127 173	Db 182 LMEDGKGCVLVRGLEEBIVTSANBIFTLLERGSAKRTABTLLNKQSSRSHSLFSI 237 Qy 229 KVDQRERLAPPRQRECKLYLIDLAGSEDNRTGNKGLRLKESGAINTSLFVLGKVVDA 286 :	Db 298 LVEHLGHIPYRDSKLTRLLINDSLGGRTKTCIIATVSPAVHCLEFTLSTLDYARRAKNIKN 357 Qy 347 RPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQK 401	451 VEEKDLEIERLKTKOKELEAKMLAQKAE 478

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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Atclesslonence unmber: A86141; MUID:21016719; PMID:11130712
A;Accesslon: B65131
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C;Genetics:
A;Map position: 1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1228, Ap Sequence 1228, Ap Sequence 90095, A Sequence 11424, A Sequence 11424, A Sequence 11425, A Sequence 6, Appli Sequence 7, Appli Sequence 2, Appli Sequence 149034, Sequence 103346, Sequence 103346, Sequence 537, Appli Sequence 10346, Sequence 537, Appli Sequence 10346, Sequence 537, Appli Sequence 10346, Sequence 537, Appli Sequence 547, Appli Seque Sequence 8784, Ap Sequence 90071, A Sequence 90071, A Sequence 90072, A Sequence 90098, A Sequence 90096, A Sequence 90096, A Sequence 90099, A Sequence 4, Appli Sequence 4, Appli Sequence 425, App Sequence 10738, A Sequence 80, Appl Sequence 80, Appl Sequence 8784, Ap Sequence 80, Appl Sequence 7228 Sequence 1670 Sequence 5160 - Bescription US-09-597-292-8
US-10-797-893-8
US-10-797-893-8
US-10-797-893-4
US-10-737-893-8
US-10-737-893-8
US-10-738-878-425
US-10-738-878-425
US-10-738-878-80
US-10-734-878-80
US-10-949-10-878-80
US-09-724-676A-90071
US-09-724-676A-90096
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US-10-797-893-2 US-09-791-537-149034 US-09-791-537-149034 US-60-182-902-537 US-60-163-233-3026 US-60-163-288-7228 US-10-438-246-16760 DB Length Query Match 22467 22467 223099 2233099 22335 22335 22335 22335 22335 22335 2141 2128.5 2128.5 2128.5 Result

ALIGNMENTS

RESULT 1 US-09-597-292-8 ; Sequence 8, Application US/09597292 ; GENERAL INFORMATION: ; APPLICANT: Beraud, Christophe ; TITLE OF INVENTION: Novel motor proteins and methods for ; TITLE OF INVENTION: their use
<pre>; FILE REFERENCE: 1044 ; CURRENT APPLICATION NUMBER: US/09/597,292</pre>
; CURRENT FILING DATE: 2000-06-20 ; PRIOR APPLICATION NUMBER: US 09/295,612
; PRIOR FILING DATE: 1999-04-20 ; NUMBER OF SEO ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SECTION OF THE PROPERTY AND SECTION OF THE PROPERTY AND SECTION OF THE PROPERTY OF THE PROPE
) ALFL: FAI Human) ORGANISM: Human US-09-597-292-8

SUMMARIES

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FastSEQ for Windows Version 4.0
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        Length 487;
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GENERAL INFORMATION:
TITLE OF INVENTION: Christophe
TITLE OF INVENTION: Howel mccor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR PILING DATE: 2000-11-26
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
STANDRER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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   ; Score 2472; DB 19;
; Pred. No. 1.3e-204;
0; Mismatches 0;
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     Query Match
Best Local Similarity 100.0%;
Matches 487; Conservative 0
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US-10-733-878-425

US-10-733-878-425

SEQUENCE 425. Application US/10733878

SEQUENCE 425. Application US/10733878

SEQUENCE 5. Application US/10733878

SECURT 6. STANCE Francis Amalric

APPLICANT: Jean-Philippe Girard

APPLICANT: Thomas Clousine

TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR

TITLE OF INVENTION: THAP PROTEINS AND ROLES IN TRANSCRIPTIONAL REGULATION

TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION

FILE REFERENCE: BIOBANK. 012A

CURRENT FILING DATE: 2003-12-10

PRIOR APPLICATION NUMBER: 60/482699

PRIOR PELICATION NUMBER: 60/485027

PRIOR PELING DATE: 2003-07-03

NUMBER OF SEQ ID NOS: 535

SEQ ID NO 425

LENGTH: 665
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99.8%; Score 2467; DB 33;
Best Local Similarity 100.0%; Pred. No. 5.9e-204;
Matches 486; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-733-878-425
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GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Wovel motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/09/724,224
PRIOR PILING DATE: 2000-11-28
PRIOR PLILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 512
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NHCPTM 512
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US-10-797-893-4
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TYPE: PRT CRGANISM: Homo sapiens PCT-US03-02234-80
    TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-41687-80
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                                                                                           APPLICANT: ADAMS. Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE REFERENCE: CL0001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SEQ ID NOS: 40312
SEQ ID NO 1038
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GENERAL INFORMATION:
APPLICANT: SUGEN, INC.
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KITASES IDENTIFIED WITH THE METHOD
FILE REPERENCE: 038602/1544
CURRENT APPLICATION NUMBER: PCT/US02/41687
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/43,169
PRIOR APPLICATION NUMBER: 60/43,169
RAIOR APPLICATION NUMBER: 60/43,169
SOFTWARE: PATCHING DATE: 2011-12-31
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PATCHING Ver. 2.1
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93.4%; Score 2309; DB 27;
Best Local Similarity 100.0%; Pred. No. 1.8e-190;
Matches 455; Conservative 0; Mismatches 0;
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                                                                    Sequence 10738, Application US/10170205E
GENERAL INFORMATION:
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506 NHCPTM 511
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10-170-205E-10738
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Sequence 80, Application PC/TUS0302234
GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR V.
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFREENCE: 038602/1571
CURRENT APPLICATION NUMBER: PCT/US03/02234
CURRENT PILING DATE: 2003-01-28
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 90.
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                                    Indels
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93.4%; Score 2309; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.8e-190;
Matches 455; Conservative 0; Mismatches 0;
Score 2309; DB 1; L
Pred. No. 1.8e-190;
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 455; Conservative 0; Mismatches
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Sequence 80, Application US/10334143

GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: MINABES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543

CURRENT APPLICATION NUMBER: 60/343,169
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR APPLICATION NUMBER: 2001-12-31
SEQUID NOS: 207
SOFTWARE: PALENTIN Ver. 2.1
SEQUID NO 802
                                                                                         394 VKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTHARE: PASESEQ for Windows Version 4.0
SEQ ID NO 8784
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93.4%; Score 2309; Di
Best Local Similarity 100.0%; Pred. No. 1.8s
Matches 455; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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                          GENERAL INFORMATION;

JAPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001107

CURRENT APPLICATION NUMBER: US/10/940,774

CURRENT FILING DATE: 2004-09-15

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 8784

LENGTH: 490

LENGTH: 490
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; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; TITLE REFERENCE: 1291814-4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90071
; LENGTH: 559
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100.0%; Pred. No. 1.8e-190;
tive 0; Mismatches 0;
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    Sequence 8784, Application US/10940774
GENERAL INFORMATION:
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Best Local Similarity
Matches 455; Conserv
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US-09-724-676-90071
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US-10-940-774-8784
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; Sequence 90071, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TILLE OF INVENTION: Variants of alternative splicing; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SEQ ID NO 90071
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Best Local Similarity 99.8%; Pred. No. 5.9e-184;
Matches 442; Conservative 1; Mismatches 0;
Score 2235; DB 21;
Pred. No. 5.9e-184;
1; Mismatches 0;
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      90.4%;
      Query Match 90.4
Best Local Similarity 99.8
Matches 442; Conservative
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CRGANISM: Homo sapiens
US-09-724-676A-90071
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Search completed: November
Job time : 299.595 secs
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US-09-724-676-90072

Sequence 90072, Application US/09724676

Sequence 90072, Application US/09724676

Tare OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION UNMERR: US/09/724,676

UNMER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

SEQ ID NO 90072
                                                                                                                                                                                                                                                                                                                                                             90.4%; Score 2235; DB 21; 99.8%; Pred. No. 6.4e-184; ative 1; Mismatches 0;
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Matches 442; Conservative
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Sequence 90072, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl:
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 97222
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CORGANISM: Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	* Query Match	* Query Match Length	DB	QI	Description	ion	
1	2472	100.0	487	7	ADC23344	Adc23344	Human k	1 12
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ADO44167 ADM04007 ADM04007 ABG70990 AAE14400 AAE14400 AAU79590 AAU79590 ADU83230 ADC35116 ADC35116 ADC9526 ADC96926 ADC96926 ADC96926 ADC96936	ALIGNMENT	487 AA.		ng protein	domain; kinesin-lik; immunomodulator; a restenosis; cellula immune disorder; in								as mc proli of the	nglish	novel met pounds fo cifically e activit t protein his activ headouts.
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20-JUN-2000; 2000US-00597292. 28-NOV-2000; 2000US-00724224.

(CYTO-) CYTOKINETICS INC

WPI; 2004-532491/51 N-PSDB; ADQ60233.

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kinesin-like DNA binding protein (known as KID) as cytostatic, cardian immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. The polypeptide sequence is human KID protein (SeqID 8) of the invention.
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restences, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular cropilitration disorders such as cancer, hyperplasias, restences, cardiac proliferation disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders such as cancer, hyperplasias, restences, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating cellular consistences are used for associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting consistences are used for proliferation induced after medical procedures including surgery and consistence in the properties and inflammatory bowel disease and and prover protein procedures including surgery and inflammatory based and consistence approaches a human microtubule motor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP
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100.0%; Pred. No. 6e-224;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 487; Conservative
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28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 4) of the invention.
SLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAEEK 480
                                                                                                                                                                                                                                                   human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a candidate agent as modulator of function of a targ
protein for treating cellular proliferation disorders by adding
candidate agent to a mixture of the target protein that
directly/indirectly produces ADP or phosphate.
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                                                                                                                                                                                                                      Human kinesin-like DNA binding protein (KID) (SeqID 4).
                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by CA"
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                               ADC23340 standard; protein; 512 AA.
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20-JUN-2000; 2000US-00597292.
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                             ENHCPTM
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                                                                                                                                                             ADC23340;
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421
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ADC23340
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                    97 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 146
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LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTWLGSPEQPG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angloplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                      267 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                          TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
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                                                                   VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                           LIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPFRO
                                                                                                                                                                            LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                              REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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                                                                                                                                                                                                                                                                                                                                                                                  387 VKLSQKELLGPPEAXRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                   LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLETERLKTKQKELEAKMLAQKAEEKE
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2000US-00597292.
2000US-00724224.
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Gaps

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Best Local Similarity 100. Matches 486; Conservative

protein SEQ ID NO:425.

Human KNSL4 23-SEP-2004

The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase for including methods of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein or act as a modulator of the binding characteristics or concer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular consistency by immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and diseases, arthritis, graft rejection, inflammatory bowel disease and angioplasty. This sequence represents a human microtubule motor procein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:3, but this does not Claim 1; SEQ ID NO 4; 26pp; English. appear to be the case.

Sequence 512 AA;

ö 146 206 241 266 301 361 TRILIQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP 386 421 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAEEKE 481 121 181 86 362 VKLSQKELLGPPEAKRARGPEEERIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 62 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEQQNASVLAYGFTGAGKTHTMLGSFEQPG VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL TRILLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP 387 VKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS 2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET Gaps . 0 Length 512; Indels 99.8%; Score 2467; DB 8; L 100.0%; Pred. No. 1.9e-223; 100.0%; Pred. ... Query Match Best Local Similarity 100.0 Matches 486; Conservative NHCPTM 487 NHCPTM 512 207 242 267 482 507 122 302 327 182 셤 g a 셤 ð 셤 à ò 원 셤 ò à 셤 ò ð à

ADQ09240 standard; protein; 665 AA.

RESULT 5 ADQ09240

ADQ09240;

The present invention describes a method for modulating the expression of a thanacos (death)-associated protein (THAP) responsive gene. The method compitation of a THAP family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing to compitating the expression of a gene responsive to a THAP responsive to complex; (2) a pharmaceutical carrier; (3) a transcription factor decoy compissing a THAP responsive element; (4) a cell method of consisting essentially of a THAP responsive element; (4) a cell compissing a transcription factor decoy described above; (5) methods of consisting a transcription factor decoy described above; (5) methods of conjugation factor decoy described above; (5) methods of conjugation of a conjugation of a conjugation of a conjugation of a conjugation of comprising a transcription factor which comprises a promoter operably linked conjugation of conjugation methods of comprising a print of constructing a cell which expresses of fragment; (7) a method of constructing a cell which expresses of fragment; (7) a method of constructing a cell which expresses of fragment; (7) a method of constructing a cell which expresses of fragment; (7) a method of constructing a cell which expresses of fragment; (7) a method of constructing a cell which expresses of fragment; (7) a method of constructing a cell which expresses of compound that modulates transcription construction methods for reducing the symptoms associated with a condition mediated by a THAP-family polypeptide in an individual; or a THAP-family polypeptide in an individual; or a conferior to the nucleus; (10) methods for reducing the symptoms associated with a condition associated with a condition resulting from the symptoms associated with a remarkation or a THAP-family polypeptide in an individual; or symptoms associated with a remarkation or a THAP-family polypeptide in an individual; (11) a method or confirming a test composition are proposited with a condition and confirming a mindipolate proposition are Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; appbrosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; encroprotective; osteopathic; THAP modulator; THAP synthesis modulator; Clouaire T; Example 47; SEQ ID NO 425; 612pp; English. Roussigne M, ENDOCUBE SAS. CNRS CENT NAT RECH SCI. 10-DEC-2002; 2002US-0432699P. 03-JUL-2003; 2003US-0485027P. 10-DEC-2003; 2003WO-IB006434. Girard J, Amalric F, WPI; 2004-525034/50. N-PSDB; ADQ09241 WO2004055050-A2 Homo sapiens. 01-JUL-2004. (ENDO-) 1 (CNRS) (

31-DEC-2002; 2002WO-US041687 31-DEC-2001; 2001US-0343169P

WO2003057841-A2.

17-JUL-2003

Homo sapiens.

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Grigoriev IV, Sudarsanam GRIGORIEV I V SUDARSANAM S.

(GRIG/) (SUDA/)

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cytostatic, neuroprotective and osteopathic activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation us useful for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAEEKE 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgeaic; hypotensive; immunoauppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dystunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
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                                                                                                                                                                                Length 665;
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                                                                                                                                                                             99.8%; Score 2467; DB 8; L 100.0%; Pred. No. 2.9e-223; .ive 0; Mismatches 0;
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                                                                                                                                                                                                            Matches 486; Conservative
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                                                                                                                                                                                             Local Similarity
                                                                                                                  present invention
                                                                                                                                                Sequence 665 AA;
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (b); (c) hybridizes under stringent conditions to (a) and complement of conformal and all, of an complement of the catalytic domain, a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, colleges, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or conversably cancers of the tissues or of hemacopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, cortain infections caused by fungi, ocular diseases, migraines, pain, bacteria, infections caused by fungi, ocular diseases, migraines, pain, coviral infections, infections caused by fungi, ocular diseases, migraines, pain, context, infections caused by fungi, ocular diseases, migraines, pain, context, infections caused by fungi, ocular diseases, migraines, pain, context, infections, infections, such and organ transplant of disorders, dyskinesias, metabolic disorders and organ transplant context, including the context of the kinase polypeptides of the criptors.
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                                                                                                                                                                                                                                                                                                                                           New isolated, enriched or purified nucleic acid molecule encoding a
kinase polypeptide, useful for treating cancer, immune-related diseases,
cardiovascular disease, brain or neuronal-associated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 80; 491pp; English.
                                                                                                                                                                                                                                                                                                     WPI; 2003-587115/55.
                                                                                                                                                                                                                                                                                                                                                                                                           metabolic disorders.
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Best Local S
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61 63 121 123 181 241 243 301 303 361 363 421

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human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                            242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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                                                                                                       LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                              VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                    4 GRCRLSKIGATRRPPFARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                             GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human kinesin-like DNA binding protein (KID) (SeqID 6).
1; Mismatches
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20-JUN-2000; 2000US-00597292.
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   Conservative
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   422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC23342;
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       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                             421
                                                                                                                    453
         361
                                                                                                     TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                 VKLSQKELLGPPEAKRARGPEEEBIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate cancer antigen protein sequence SEQ ID NO:1228.
                                                                                                                                                                              LDRILLASQGSQGAPLLSTPKRERMVLMKTVEEKDL 456
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                                                                                                                                                                                                                                                                                             AAB56650 standard; protein; 460
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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such as prostate cancer.
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N-PSDB; AAF15853.
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WO200055174-A1.

Homo

13-MAR-2001

AAB56650

RESULT

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12-MAR-1999;

Length 460;

Score 2141; DB 3; Pred. No. 9.6e-193;

86.6%;

Query Match Best Local Similarity Seguence 460 AA;

invention

us-10-797-893-8.rag

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ADC23338 standard; protein; 370
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                                                                                                                                                    inflammation.
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Best Local Simi
Matches 346;
                                           Beraud C;
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                       This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 6) of the invention.
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                                                                                                                                                                                                                                                                                                               1 MGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQE
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                                                                                                                                                                                                                                         71.5%; Score 1768; DB 7; 100.0%; Pred. No. 1e-157; ive 0; Mismatches 0
Claim 1; SEQ ID NO 6; 26pp; English.
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28-NOV-2000; 2000US-00724224.
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Best Local Similarity 100.
Matches 346; Conservative
                                                                                                                                                                                                                 Sequence 346 AA;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening cor modulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune confiseration induced after rediction, inflammatory bowel disease and proliferation induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein contents and man and man and motor protein and contents and method and method and microtubule motor protein contents and method and 
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100.0%; Pred. No. 1e-157;
iive 0; Mismatches 0;
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(CYTO-) CYTOKINETICS INC.
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N-PSDB; ADQ60231.
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human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                          Identifying a candidate agent as modulator of function of a targ protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
      Human kinesin-like DNA binding protein (KID) (SeqID 2).
                                                                                                                                                                                                        20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
                                                                                                                                                                                     28-NOV-2000; 2000US-00724224
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                                                                                   Homo sapiens
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/note= "Encoded by ATGCA"

Location/Qualifiers

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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using or phosphate. Furthermore readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antinfinammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 2) of the invention.
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Claim 1; SEQ ID NO 2; 26pp; English.
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Matches 345; Conserv
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening cardial encoding them. The invention also relates to a method of screening for medulators of a microtubule etimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenoisis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA conditions of the cardiac for the inflammation of the cardiac for proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenois, cardiac hypertrophy, immune disorders and inflammation, for treating disorders hypertrophy, immune disorders and inflammation, for treating disorders consociated with KID and for inhibiting KID and for treating disorders and inflammatory bowel disease and proliferation induced after medical procedures including surgery and construction protein, inflammatory bowel disease and proliferation induced after medical procedures including surgery and construction protein motor protein cof the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:1, but this does not

Claim 1; SEQ ID NO 2; 26pp; English

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Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                               TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN
                                                                                                                                                             Human microtubule motor protein #1.
                                                                                                       ADQ60228 standard; protein; 370
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                    :||| : || || || || || 5 SRRPGIGSSQIPNECVQVVVRCRPMSNRERSERSPEVVNVYPNRGV----VELQNVVDGN
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           ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                 TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLBIANW--RN
                                                                                                                                                                                                                                                                                                                   REDCRGN-ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQ
                                                                                                                                                                                                                                                                                                                                                                        233 RERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                             293 RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLQPHALGPVKLSQ------KELLGPPEAKRA-------RGPEEEEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APLLSTPKRERMVLMKTVEEKDLEIER-----LKTKQKELEAKMLAQKAEE
                                                                                              Length 784;
                                                                                           ; Score 616; DB 4; Length 78;
; Pred. No. 2.1e-48;
84; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 22341
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                                                                                             24.9%;
33.1%;
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2000US-00614150.
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                                                                                        Query Match
Best Local Similarity 33.1%
Matches 176; Conservative
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                                                                   Sequence 784 AA;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                    REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL 301
                                                                                                                                                                                                                                                                                                     266 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL 325
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                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                     LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                             LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                              GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                   GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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            Length 370;
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                                   Indels
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                         3.3e-157;
            DB 8;
                                     Mismatches
          Score 1763;
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                         Pred. No.
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71.3%; Scor.
100.0%; Pre
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11-JUL-2000; 2000US-00614150
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                                     Conservative
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                      Similarity
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human kinase protein #33.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                       20 VRVAVRLRPFVDG--TAGASDPPCVRGMD-SCSLEIANWRNHQETLKYQFDAFYGERSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP---GVIPRALMDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 LOLTREEGAEGREWALSVTMSYLEIYOEKVLDLLDPASG-DLVIREDCRGNILIPGLSOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 PISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPFRO--REGKLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 LVDLAGSERQSKTQASGQRLKRATKINLSLSVLGNVISALVDGKSTHIPYRNSKLTRLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 KLSOKEL-LGPPEAKRARGPEEEIGSPEPMAAPASASOKLSPLOKLSSMDPAMLERLLS
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                              Disclosure; SEQ ID NO 22341; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                              Length 677;
                                                                                                                                                                                                                                                                                                                                                24.0%; Score 593; DB 4; Length 67
33.9%; Pred. No. 2.5e-46;
ive 78; Mismatches 190; Indels
Myers EW;
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   PWD,
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GGENLLEKAQTQE 486
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Best Local Similarity 33.9%
Matches 167; Conservative
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   Venter JC, Adams M,
                                            N-PSDB; ABL09286
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and cencedes a naturally occurring kinase polypeptide; (d) encodes the concept that it lacks one or more, but not all, of an oplypeptide in (a), except that it lacks one or more, but not all, of an or N-terminal domain, c-terminal catalytic domain, a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, commune-related diseases and metabolic disorders. The disorders are neuronal-associated diseases, and metabolic disorders are for eneuronal-associated diseases, and metabolic disorders diseases, control or peripheral nervous system, Alzheimer's diseases of the central or peripheral nervous system, Alzheimer's diseases of the central infections caused by fungi, ocular diseases, migraines, pain, carceria, infections caused by fungi, ocular diseases, migraines, pain, diseases, midretion, mood disorders, attention disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant crejection. This sequence corresponds to one of the kinase polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated, enriched or purified nucleic acid molecule encoding a
kinase polypeptide, useful for treating cancer, immune-related diseases,
cardiovascular disease, brain or neuronal-associated diseases and
                           cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian, virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; pain; sexual dysfunction; mod disorder; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grigoriev IV,
                                                                                                                                                                                                                                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide (a) comprising any the 666 fully defined nucleotide sequences appearing as ADD49269 - ADD49935, ADD49936 and ADD49938, complements of (a); sequences of at least 20 contiguous residues (a); sequences that hybridise to (a) under highly stringent conditions; sequences having at least 75 or 90% identity to (a); or degenerate variants of (a). Also included are an isolated polypeptide ((b) (comprising: sequences encoded by the new
                                                                                                                            SPRSKLHLVDLAGSERQKKTKAEGDRLKEGININRGLLCLGNVISALGDDKKGSFVPYRD
              IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIREDCRGN
                                                     ILIPGLSQKP1SSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR
                                                                                                            OREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVIGKVVDALNQGLPR--VPYRD
                                                                                                                                                                      SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA
                                                                                                                                                                                                                           LGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLER
                                                                                                                                                                                                                                                         AELINHLKQ------LOSLMEINOLLLQAHGGTLPGSINAEPSEN---LOSLMEINOSLVEE
                                                                                                                                                                                                                                                                                  LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-ELEAKMLAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polypeptides and polynucleotides useful for diagnosing, preventing and treating cancer, particularly lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; lung cancer antigen; cytostatic; lung cancer; gene therapy;
vaccine; T-cell; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lung specific tumour antigen L 1447p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 670; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD49938 standard; protein; 1232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-2002; 2002US-00116712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2001; 2001US-0282289P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-844452/78.
N-PSDB; ADD49936.
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polynucleotide, any of the 4 amino acid sequences fully defined in the specification; or sequences having at least 70 or 90% identity to the sequence in (a) or (b)), an expression vector comprising the above captered in (a) or (b)), an expression vector comprising the above polymucleotide operably linked to an expression control sequence, a not isolated antibody, or its antigen-binding fragment, that specifically a solve-emtrioned mucleotide sequences under highly stringent conditions, a twist to protein comprising at least one polymeptide cited above, detecting the presence of a cancer in a patient (comprising) obtaining a biological sample from the patient; contacting the biological sample from the patient; or an amount of the polymeptide cited above, detecting in the sample an amount of a polymeptide cited above, detecting in the sample an amount of a polymeptide cited above, detecting in the sample an amount of a polymeptide cited above, the binding agent, or an amount of a polymelectide that hybridises to the binding agent, or an amount of a polymelectide that hybridises to the binding agent, or an amount of a polymelectide that hybridises to the oligonuclectide; and comparing the presence of a cancer in the polymuclectide that hybridises to the oligonuclectide to permit the above composition and or a tumour protein (comprising contacting T-cells with the above composition and a second component selected from the above composition protein. The patient the above composition protein comprising administering to the patient the above and a second component selected from physiological carriers and antigen presenting cells that e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRVALRCRPLVPKEISEGCOMCLSFVPG----EPQVVVGTDK-----SF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.2%; Score 574.5; DB 7; Length llarity 32.5%; Pred. No. 3.6e-44; Conservative 97; Mismatches 161; Indels
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Matches 160; Conserv
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MDPAMLERLISLDRILASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-EL

411

391 KNQSLVEENEKLSRGLSEAAGQTAQML----ERIILTEQANEKMNAKLEELRQHAACKL 445 Ωp

469 EAKMLAQKAEEKE 481 ::|::| 446 DLQKLVETLEDQE 458

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Search completed: November 5, 2004, 18:44:42 Job time : 101.956 secs

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CR615781 full-leng
CR590974 full-leng
AL545712 AL545712
CR590954 full-leng
BX337406 BX337406
AL559772 AL559772
BX337353 BX337353
BX3635466 BX354166
AL559769 AL559769
BX376199 BX376199
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BM546877 AGENCOURT
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AGENCOURT
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AL555550 A
CD109092 A
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GenCore version 5.1.6.
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BX354166
AL559769
BX376199
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BX376199
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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7.00	CR615781 full-length cDNA clone C of Homo sapiens (human). CR615781.1 GI:50496588 HTC; CNSLT cDNA. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Li,W B., Gruber, C., Jess Full-length cDNA librari Unpublished Contact : Feng Liang Ema http://fulllength.invitr. Faraday Avenue Contact : Feng Liang Ema http://fulllength.invitr. Faraday Avenue Submitted (20-JUL-2004) Submitted (20-JUL-2004) BP 191 91006 EVRY cedex Web : www.genoscope.cn list strand cDNA was prim end enriched, double-str into the Not I and Ecok was normalized. Library division of Invitrogen: Location/Qualifa	1.
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Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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full-length cDNA clone CSODI009YJ01 of Placenta Cot 25-normalized
one flow sapiens (human).
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Catarrhini, Hominidae, Homo.
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1. 2025
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_Xref="taxon:9606"
/clone="CSOD1009y01"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                          Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 2025)
                                                                                                                            CR590974.1 GI:50471781
HTC: CNSLT_CDNA.
Homo sapiens (human)
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/organism="Homo sapiens"
/mol_type="mRNA"
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/dboxe="taxon:9606"
/clone="CSODIODYJO1"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI009CE01QP1&c=7766. Location/Qualifiers
   was normalized. Library was constructed by Life Technologi
division of Invitrogen. This sequence belongs to sequence
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Matches 1059; Conservative
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BP 191 91006 EVRY cedex - France
BM 11: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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1 (Bases 1 to 1124)

1i, W.B., Gruber, C., Jessee, J. and Polayes, D.

1i, W.B., Gruber, C., Jessee, J. and Polayes, D.

1by Mannellian (2001)

On Reb 15, 2001 this sequence version replaced gi:31267547.

Contact: Genoscope
                   GATCCCGCGGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGGGCGCCGAGGGCCG
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GATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGTGCCGAGGGCCG
                                                                                    CCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATCCT
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TITLE
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                                                                                         CCCCCTGTGTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAACCACC
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 GENYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 9100 GENYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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                                                AGAGGGAAAACTCTACCTGATTGACTTGGCTGGGKCAGAGGRCAACCGGSGCACAGGCAA 840
                                                                                           CAAGGGCCTTCGGCT-AAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCA 918
                                                                                                           AAGTGGTAGATGCGCTGAATCAGGGCCTCCTCGTGTACCTTATCGGGACAGCACAAGCTCA 978
 TCATGCTGTGCTCCTGGTCAAGGKGGACCAGCGGRACGTTTGGCCCCATTTCGCCAGCG 780
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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2016)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished
                                                                                                                                                                        AAGTGGTAGATGGGCTGAATCAGGGSCTCCCTCGTGTACCTTATCGGGRCAGCTCA
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                                AGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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Pred. No. 1.5e-276;
0; Mismatches 1; Indels 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI040Y106"
/tissue_type="Placenta Cot 25
/plasmid="pCWVSPORT_6"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1083)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

3 Full-length CDNA libraries and normalization

3 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

4 Full-length CDNA libraries and normalization

4 Inpublished (2001)

5 Full-length CDNA libraries and normalization

5 Contact: Genoscope

6 Genoscope - Centre National de Sequencage

8 BP 191 91006 EVRY cedex - France

8 Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

8 Extrand CDNA was primed with a NotI-oligo(dT) primer. Five prime

9 enriched, double-strand CDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 7766.r

For more information about this cluster, see
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                                                TCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAGACCTCCTGGACCCTGCTT
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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1027 bp mRNA linear EST 07-APR-200-BX337406 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI041YII3 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAGGCACTIGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGGACCCACAGGAGCTG 396
                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1027)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30341614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/clone="SODI041Y113"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone=lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                         BX337406.2 GI:46274820
                                                                                                                                                   Homo sapiens (human)
Homo sapiens
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960

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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX337353 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI040Y106 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                      970 GCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTG 1029
                                                                                                                                                                                                                                                                                                                                                                     961 GCAACTCACTYCGCCTATTGCA-GRCTCTCTGGGTGGSTCACCCMAGTAT---CYTATTG 1016
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominid
1 (bases 1 to 1032)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
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llarity 98.6%; Pred. No. 1e-258;
Conservative 4; Mismatches 8;
TTCGCCAGCGAGGGAAACTCTACCTGATTGACTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |: | || :|:|| | | || 1017 CAMATIGCCCTKARARAGCTTYTHCTA 1044
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/clone="CS0DI040Y106"
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Homo sapiens
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| db_xref="texon:9606"
| folone="CSOBGG05YLII" | RAMOS CELL LINE) | |
| fissue type="B CELLS (RAMOS CELL LINE) | |
| folone lib="Homo sapiens B CELLS (RAMOS CELL LINE) | |
| folone lib="textor: pcWvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, the Not I and SCRAV sites of the pCMvSPORT 6 vector. Library was not normalized."
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                                                                                                   'organism="Homo sapiens"
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For more information about this cluster, see
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AGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACA
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/cell type="HELA CELLS COT 25-NORMALIZED"
/cell line="HELA"
/clone lib="Homo sapiens HELA CELLS COT 25-NORWALIZED"
/note="HELA strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODK012YE23"

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                                Gaps
                                ;
 Length 959;
                               0; Indels
 Score .942; DB 5; I
Pred. No. 1.3e-248;
0; Mismatches 0;
Query Match
Best Local Similarity 99.9%;
Matches 953; Conservative
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BX363358 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK012YE23 5-PRIME, mRNA sequence.

DEFINITION

BX363358.2 .GI:46287820 EST. sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE

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                                                                     Indels
                  Score 934; DB 5; I
Pred. No. 2.1e-246;
0; Mismatches 0;
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Matches 956; Conservative
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Br 191 91006 ENYZ cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

1st strand CDNA was primed with a NotI-oligo(dT) primer. Prime prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
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BX354166
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1 (Dases 1 to 958)
1 iv.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30373827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGAAGGTATTAGACCTCCTGGACCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTG
                                                                                                                                                                                         CCGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTT
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GGGTGCCGAGGGCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCA
                                                     <u>GGAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTG</u>
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Contact: Genoscope
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BX354166
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 1094)

2 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

L. Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30452476.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX376199 1000 sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODC024YAl0 5-PRIME, mRNA sequence.
                                                                                                 GAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAG
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                                                                    GAGCAACCTGGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAG
                                                                                                                                                                                 GGTGCCGAGGGCCGATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAG
                                                                                                                                                                                                                                                                                               GAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGC
                                                                                                                                                                                                                                                                                                                                           581 GAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGAGACCTGGTAATCCGAGAAGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 CGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAGCCCATCAGTAGCTTTGCTGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAGGGCYTCC 983
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSODC024YA10"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCRVNSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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ALS59769 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
clone CSODG005YP11 5-PRIME, mRNA sequence.
ALS59769
                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li, Ma.B.; Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
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This sequence belongs to sequence cluster 7766.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DG005cC06QP1&c=7766.r.
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                                                                                                                AL559769.3 GI:46185141
                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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/organism="Homo sapiens"
/mol type="mRNA"
/db_ref="taxon:9606"
/db_ref="taxon:9606"
/clone="IMAGE:545401"
/tissue_type="astrocytoma grade IV, cell line"
/lab_host="BilloB (phage-resistant)"
/clone_lib="NIH MGC:98"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
ECGRI; cDNA made by oligo-dr priming. Directionally
cloned into BcoR/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                     AGENCOURT 6702754 NIH MGC 98 Homo sapiens cDNA clone IMAGE:5454101
57, mRNA Sequence.
BM910587
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1031)
S NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
C Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCGN1948 row: I column: 06
High quality sequence stop: 679.
                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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GGAGCAAGTGATCCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAAC
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Pred. No. 1e-241;
0; Mismatches 7; Indels 1
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Matches 931; Conservative
                                                                          974
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                                                                                                                      970 GGGACAGCAAS
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    /tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
//clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
//note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                GATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATCCCCCTGTGTGCGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTGCCGAGGCCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCA 544
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                                                                                                                                                                                                                                         4;
                                                                                                                                                                                            Length 1094;
                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                       Score 921.4; DB 5;
Pred. No. 6.4e-243;
4; Mismatches 0;
                                                                                                                                                                                            82.6%;
99.2%;
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Best Local Simil
Matches 963; C
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BP 191 91006 EVRY cedex - France
BE 191 91006 EVRY cedex - France
BE 191 91006 EVRY cedex - France
BE 191 91006 EVRY cedex - France
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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sapiens
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/note="let strand cDNA was primed with a NotI-Oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGCGGCTCGACGCAGCAGCGAGCGAGATGGCGGCGCAGCTTCAGCGGCGGCGATCT
                                                          CAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCTCCTGTTTGTCCTGGGCAA
                                                                                                                                                                                                                                   AGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTA-CCTTATCGGGACAGCAA-GCTC
                                                                                                                                                                                                                                                    AGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODK002CA10QP1&c=7766.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           mRNA linear EST
COT 25-NORMALIZED Homo
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="HELA_CELLS_COT_25-NORMALIZED"
/cell_line="HELA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 907.8; DB 5;
Pred. No. 3.5e-239;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                              ACTCGCCTATTGCA-GGACTCTCTGGGTGG 1006
                                                                                                                                                                                                                                                                                                                                                                                                           BX400806 978 bp
BX400806 Homo sapiens HELA CELLS (
cDNA clone CSODK002YB19 5-PRIME, i
BX400806 GI:46845770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK002YB19"
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99.2%;
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Homo sapiens
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EST

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

DEFINITION

ACCESSION

RESULT 14 BX400806

609 596 699 929 729 716 789 776 849 836 606 896

967 955

951;

Matches

Query Match Best Local 8

ORIGIN

10

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Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

In (bases 1 to 1016)

Li, W.B., Gruber.

Li, Meb.

L
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/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="texon:9606"
/clone="CSODA009YD01"
/tissue_type="NEUROBLASTOMA"
/clone="lb="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGTAAGGGTGGCTGTGCGCGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                GGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGC
                                                                  CCTCCCGCAGTCATGCTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCAT
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Search completed: November 10, 2004, 18:18:00 Job time : 3883.13 secs

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Abs57215 Human kin Adys5077 Novel NOV Adi39619 DNA encod Adm81051 Human Hek Abt40796 Toxicity Abq73061 Human kin Adi56806 DNA encod Abd66785 DNA encod Abd66787 DNA encod Abd66787 DNA encod Abd66787 DNA encod Adb66787 Human nov Adc30858 Human NOV Adc10189 Human NOV Abl16732 Drosophil

Add19012 Human sof Aad28869 Human kin Ad198085 Novel Nov Ab128591 Drosophil Aah89871 Human bon

80

Minimum Maximum Database :

OM nucleic

Run on

Sequence:

Perfect

Searched:

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/*tag="a"/
/product= "KID protein"
/product= "KID protein"
/product= "content of transl_except= (post: 1.5; aa: Met)
/note= "This codon has an apparent 2 nucleotide insertion
that alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                        ADJ95085
ABL28591
                                                                                                                                                                                                                                                                                                                                      AAH89871
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20-JUN-2000; 2000US-00597292,
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P-PSDB; ADC23338.
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Adg60229 Human mic
Adg09241 Human KNS
Adk40995 Novel hum
Adk40995 Novel hum
Adc23341 Buman pro
Adc23341 Buman pro
Adc23341 Buman mic
Adg60231 Human mic
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Adg60234 Human gen
Ach71408 Human gen
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Aba94616 Nucleotid
Abs57216 DNA encod
Aba94614 Human kin
                                                                                              9, 2004, 09:45:10 ; Search time 576.523 Seconds (without alignments) 10152.424 Million cell updates/sec
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                                                                                                                                                                                       atgcagccgcgggcggctcg......ccaaggaggtgatcaattga 1115
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            5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             4134886 seqs, 2624710521 residues
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             GenCore version
Copyright (c) 1993 - 2004
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Listing first 45 summaries
                                                                       sw model
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ADQ60231
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Gapop 10.0 , Gapext 1.0
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genesequ2002as: *
genesequ2003as: *
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genesequ2003as: *
genesequ2003as: *
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Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that

ABA94616 ABS57216 ABA94614

Result Š

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ACCAGCGCTCCTCCCGCAGTCATGCTGTGCTCTGGTCAAGGTGGACCAGCGGGAACGTT
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                                                                                               proliferation disorders. Specifically, it refers to candidate agents that proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 1) encoding a full length KID enzyme of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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  directly/indirectly produces ADP or phosphate.
                                                                                  to a novel method
                                       Disclosure; SEQ ID NO 1; 26pp; English
                                                                                  invention relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       961 ATCGGGACAGCACACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA
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activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, and act as a modulator of the binding characteristics or biological activity of a traget protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders and inflammation, for treating cellular proliferation disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune disorders are associated with KID and for inhibiting KID and for treating autoimmune disorders are proliferation induced after medical procedures including surgery and angioplasty. This sequence respected by especification states that this motor protein of the invention. Note: The specification states that this armain the properties of the protein featured as SEQ ID NO:2, but this does not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl except= (pos: 4. .5; aa: Pro)
/note= "This codon has an apparent 1 nucleotide deletion
that alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                   TGGCCCCATTTCGCCAGCGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGG
                                                                                                                                        ACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGGGCCATCAACACCT
                                                                                                                                                                                                                                                                                                                               TCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCA
ACCAGCGCTCCTCCCCCCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTT
                                                                                                                                                                                                               CCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCTCGTGTACCTT
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                                                                                                                  ACAACCGGCGCACAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCT
                                                                                                                                                                                      Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                       1081 ACTITGCTGCCAGGTCCAAGGAGGTGATTGA 1115
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20-JUN-2000; 2000US-00597292.
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ACCAGCGCTCCTCCCGCAGTCATGCTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTT
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20-JUN-2000; 2000US-00597292.
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                                     CC This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular CC proliferation disorders. Specifically, it refers to candidate agents that are appable of modulating the activity of target proteins having motor CC domains, such that the target protein directly produces ADP CC or phosphate. Furthermore, this activity can be determined using cor phosphate. Furthermore, this activity can be determined using method that identifies modulators of the target protein, which is a ckinesin-like DDA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene contact the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 3) encoding a full length CKID enzyme of the invention.
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Pred. No. 1.1e-310;
0; Mismatches 1; Indels
    or phosphate
                         Disclosure; SEQ ID NO 3; 26pp; English
    produces ADP
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Matches 1113; Conservative
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                                                                                                                                                                                                                                                                                        arthritis;
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activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune chieses, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and angloplasty. This sequence represents DNA encoding a human microtubule motor protein of the invention. Note: The specification states that this angles and angles angles and angles angles and angles and angles ang
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1538 BP; 355 A; 432 C; 459 G; 292 T; 0 U; 0 Other;
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Matches 1113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for modulating the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis is cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
                                                                        ACAACCGGCGCACAGGCAACAAGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCT
                721 ACCAGGGCTCCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACGTT
                                                                                                                                                                                         ATCGGGACAGCACCCCCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA
                                                                                                                                                                                                                                                                                                                 TCCTTATTGCCAACATTGCCCCTGAGAGGCCTTCTACCTAGACACAGTCTCCGCACTCA
                                                      TGCCCCCATTTCGCCAGCGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGG
                                                                                                               ACAACCGGCGCACAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCT
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a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing biological fragment with a nucleic acid, and so enhancing or repressing comprises modulating the expression of a gene responsive to a THAP (hemokine complex; (2) a pharmaceutical carrier; (3) a transcription factor decoy consisting a transcription factor decoy described above; (5) methods or comprising a transcription between a nucleic acid and a THAP-family or pryeptide or its biological fragment, or a nucleic acid and a THAP-family or pryeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell inne comprising a THAP-family polypeptide or its biological a transcription a prical vector packaging cell line comprising a transcription or transcription a transcription a prical vector packaging cell line comprision or a THAP-family polypeptide; (8) a method of constructing a cell which expresses a combination that the nucleus; (10) methods for radioristing a test compound that modulates transcription at a THAP responsive element or that modulates the transcription at any papercessive or insufficient apoptosis, inflammation, metatestasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovaccular disease and neurodegenerative activity of a chemokine or a THAP-family polypeptide in an individual; (11) a vector comprising a theretable product; (12) a genetically engineed correct described above or that expression or activation comprising a theretable product; (12) agencially in soluted much transcription or cardiovaccular comprising a multiple or its biological fragment; (13) a method or transcription comprising a multiple or its biological fragment; (13) a method or transcription comprising a multiple or it

Sequence 2097 BP; 483 A; 592 C; 628 G; 394 T; 0 U; 0 Other;

ö GACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCC 365 245 ATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCA 125 207 GATCCCCCCTGTGTGCGGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAAC 267 caccaddaddrercreaaraccadrirdardccrircrarddddaddaddrercreaddd 327 CACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGAGAGGAGGAGTACTCAGGGG GCCGCGGGCGGCTCGACGCAGCAGGCGACGAGATGGCGGCAGCTTCAGCGGCGGCG GATCCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAAC Gaps 99.3%; Score 1107.4; DB 12; Length 2097; 99.9%; Pred. No. 3.4e-309; ive 0; Mismatches 1; Indels 0; C Conservative Similarity Best Local Simi Matches 1108; φ 99 88 208 246 268 306 148 186 126 Query Match ద g 셤 ò 셤 à g ò à ઠ

1025 965 665 725 747 785 807 845 867 905 927 987 425 447 485 507 545 567 605 627 687 cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide, ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; GACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTT GGTGCCGAGGGCCGATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAG 508 GGTGCCGAGGCCCGCCCATTTCTGTCACCATGTCTTACCTAGGATCTACCAG CGGGGGAATATCCTGATTCCGGGTCTCTCCCCAGAAGCCCATCAGTAGCTTTCCTGATTTT 688 GAGCGCCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAG CGCTCCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGAACGTTTGGCC 748 cécrécricececaércarécrérécrécrésreaageresaceaécessaacerrisece CCATTTCGCCAGCGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAAC ccarriceccaeceaegegaaaacrcraccrearreacrreecreecreegrcaegeaaac CGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTG rrigicciosecanastestasaresectenareasecticetestasecrinares GACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTT ATTGCCAACATTGCCCCTGAGAGGCGCTTCTACCTAGACACAGTCTCCGCACTCAACTTT GAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAG GAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGC 568 GAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGC CGGGGGAATATCCTGGGTCTCTCCCAGAAGCCCCATCAGTAGCTTTGCTGATTTT GCTGCCAGGTCCAAGGAGGTGATCAATCG 1136 GCTGCCAGGTCCAAGGAGGTGATCAATTG 1114 ADK40995 standard; DNA; 2099 Novel human kinase gene #15. 06-MAY-2004 (first entry) 546 909 628 808 846 868 906 928 996 1026 1108 ADK40995; 486 999 726 426 ADK40995 RESULT g 엄 셤 ò g ò g ð ద ઠ 원 ò g ð 원 ò g ò g ò ò ò

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                                              GACATCTATGCAGGTTCAGTGCAGCCCATCTAAGGCACTTGCTGGAAGGCAGAATGCC
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                                                                       389 AGTGTGCTTGCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (a); (c) hybridizes under stringent conditions to (a) and conditions to (b) peoply of the conditions of an in (a), except that it lacks one or more, but not all, of an CC terminal domain, a coiled-coil structure region, a spacer region and a CC terminal domain, a coiled-coil structure region, a spacer region and a CC terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or curronal-associated diseases, and metabolic disorders. The disorders are CC the central or peripheral nervous system, Alzheimer's disease, brain, control or peripheral nervous system, Alzheimer's disease, brain, control infections aultiple sclerosis, amyotrophic lateral sclerosis, viral infections caused by fungi, ocular diseases, miscretion, mood disorders, attention disorders, contition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant control the creaters.
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kinase polypeptide, useful for treating cancer, immune-related diseases,
cardiovascular disease, brain or neuronal-associated diseases and
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    dB,
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metabolic disorder; organ transplant rejection; enzyme; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 33; SEQ ID NO 102; 491pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase polypeptides of the invention
                                                                                                                                                                      31-DEC-2002; 2002WO-US041687
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SUDARSANAM S.
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Matches 1108; Conserv
                                                                                  WO2003057841-A2.
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ACCTGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGTGC
                                                                                                                                                   TCGCCAGCGAGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCG
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB50303 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
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 pulmonary; cardiovascular; proliferative disorder;
disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 805-806; 2338pp; English.
                                                                                                                                                              08-MAR-2000; 2000WO-US005988
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       gastrointestinal; wound; infectious
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                                                                                            WO200055174-A1.
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Best Local Similarity 100.0%; Pred. No. 2.9
Matches 1038; Conservative 0; Mismatches
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28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                   This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunoomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynuclectide sequence is human KID DNA (SeqID 7) encoding a full length KID enzyme of the invention.
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                                                                                      Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.9%; Score 1035.4; DB 10; Length 1464; 99.9%; Pred. No. 1.9e-288; ive 0; Mismatches 1; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                                  Disclosure; SEQ ID NO 7; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.9
Matches 1036; Conservative
                                 2003-706919/67.
                                                      PSDB; ADC23344.
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or bloiogical activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders condinifialmmation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating callular condisorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with kID and for inhibiting KID and for treating autoimmune consisted with kinesin induced after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubule contraction of the invention.
               New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                                                                   Disclosure; SEQ ID NO 7; 26pp; English
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Gaps 92.9%; Score 1035.4; DB 12; Length 1464; 99.9%; Pred. No. 1.9e-288; ive 0; Mismatches 1; Indels 0; 0 Best Local Similarity 99.9 Matches 1036, Conservative Query Match

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Claim 1; SEQ ID NO 31705; 44pp; English.

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by Pybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences care useful in diagnostics as expressed sequence tags (SST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probbes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisease DNA or RNA. The purified polypeptide is useful for generating antisease DNA or RNA. The purified polypeptide is useful for generating antisease of sequences. Note: The greent sequence is useful and isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 464 BP; 96 A; 136 C; 131 G; 96 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html?DocID=20030073623
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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12

(RANK/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

03-APR-2002; 2002US-00029386 03-APR-2002; 2002US-00029386

US2003194704-A1 16-OCT-2003. Claim 15; SEQ ID NO 10603; 80pp; English,

surveying tissues.

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragaments, and esquences in the specification, or their complements or fragaments, and encoding at least 8 amino acids of any of the 6888 amino acids agequences (C fully defined in the specification. The probe is a single axon probe that whytidises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule compared by solatable or amplifiable from the plurality, a single company human gene expression, a method of an addressably storession, a vector comprising the single exon probe cited above, where each of the plurality of probes is separately and pene expression, a wector comprising the single exon probe cited above, and solated antibody that binds specifically to a peptide cited above, and contiguous amino acids of any of the above mentioned amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, acustomer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable contradus methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a contain their cord including data on the expression of a single exon microarrays. C ited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying c trisques to detect the presence of expression of a single exon microarrays. In addition, the probes are useful indentifying and characterising single exon probe of the invention. Note: The sequence data for this endits and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        818 GATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAA 877
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Pred. No. 8e-57;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 531 BP; 117 A; 153 C; 149 G; 112 T; 0 U; 0 Other;
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98.7%;
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alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived single exon probe #10603.
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Нишап депоше

29-JUL-2004

ACH77408;

RESULT 13

Homo sapiens

Gaps

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide accomprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences [ully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid molecule comprising a plurality of probes for measuring human center expression, a method of and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon corriguous amino acide of any of the above-mentioned amino acide of any of the above-mentioned amino acide of any of the above-mentioned amino acide of soluted antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human apene expression data by subscription, and a computer-readable corrage medium which contains a database having a plurality of records corted above. The probes, methods and apparatus are useful in gene corrage medium which contains a database having a plurality of records cited above. The probes, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays.
AGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA 937
                       New human genome-derived single exon nucleic acid probes useful for hums gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                             TCAGGGCCTCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGAC 995
                                                                                                      Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                  Human genome derived single exon probe #24303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 24303; 80pp; English.
                                                                                                                                                                                                                              ACH91108 standard; DNA; 232 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                             (first entry)
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
                                                                                                                                                                                                                                                        821
                                                                                                                                                                                                                                                                                                                   881
                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                941
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                                                                                                                                                                                                                                                                                                                                     882 AGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAG
                                                                                                                                                                                                                                                       GTGGACCAGCGGGAAACGTTTTGGCCCAGTTTCGCCAGCGAGAGAAAACTCTACCTGATT
                                                                                                                                                                                                                                                                                   1 drdcaccadedaaacdrragececcarrregecadagagaaaacreracraarr
                                                                                                                                                                                                                                                                                                                   822 GACTTGGCTGGGTCAGAGGACAACGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GGCCTCCCTCGTGTACCTTATCGGACAGCAGCAGCTCACTCGCCTATTGCAGG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                         ;
                                                                                                                                                                                             DB 12; Length-232;
                                                                                                                                                                                                                           1; Indels
                                                                                                                                                             Sequence 232 BP; 55 A; 64 C; 68 G; 45 T; 0 U; 0 Other;
                                                                                                                               segdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                             230.4; DB 1;
No. 3.6e-56;
                                                                                                                                                                                             ; Score 230.4; I
; Pred. No. 3.6e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA of the invention SEQ ID NO:249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 249; 305pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2002; 2002JP-00137785.
                                                                                                                                                                                               20.7%;
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                                                                                                                                                                                                                    Best Local Similary
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-723558/69.
P-PSDB; ADM04007.
                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 GIGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGGA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGTGATC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAGAGGTATTAGACCTC 563
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as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM03154 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCACAGGCTGTGGGAAAACCTACCATGCTGGGCACAGACCAGGAGCCTGGCATCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCCTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 2095;
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                                                                                                                                                                                                                                                                                                      Sequence 2095 BP; 489 A; 603 C; 658 G; 345 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         Score 184.6; DB 11; Length
Pred. No. 1.6e-42;
0; Mismatches 379; Indels
                                                                                                                                                                                                                                                                                                                                                                         16.6%;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.7
Matches 463; Conservative
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Search completed: November 10, 2004, 06:57:50 Job time : 582.523 secs

1116 1056 1091 AAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCC 1031 917 936 971 966 CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCCACAGGC 857 AATCGTGGGCAGCGTATGAAGGAGGGGCCCACATCAACCGCTCACTGCTGGCACTGGGC AAAGTGGTAGATGCGCTG----AATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGC AACTGCATCAACGCCCTGAGCGACAAGGGTAGCAACAAGTACATCAACTATCGCGACAGC AACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCTCCTGTTTGTCCTGGGC AAGCTCACCCGGCTCCTGAAGGACTCTCTGGGAAGAAAAAAGAGCGCACAGTGATGATCGCT AACATTGCCCCTGAGAGGCGCTTCTACCTAGACACAGTCTCCGCACTCTAACTTTGCTGCC 1057 CACATCAGTCCTGCGAGCAGTGCCTTCGAGGAGTCCCGGAACACCCTGACCTACGCCGGC AGGTCCAAGGAGGTGATCAATTG 1114 1117 CGGCCAAGAACATTAAGACTAG 1139 817 1032 798 828 877 918 937 972 997

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BD 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized, Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             2016 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI040YI06 of Placenta Cot 25-normalized of Enon sapiens (human).
                                                                                                                                                                                                                     BX387403
AGENCOURT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens
bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2016)
1 (bases 1 to 2016)
1 (bases 1 to 2016)
Full-length cDNA libraries and normalization
Unpublished
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                                                                              AGENCOURT
                                                                                              AL576578
AGENCOURT
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BX404325
                                               BX404364
                                                                                                                                                                                                                                                        BX445789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                             BX404364
BM478215
BC555445
BM546897
BM546897
BM546897
BM546897
BM546891
BM3372162
BM3372162
BM3372162
BM3372162
BM337403
BM458841
ALS559621
BM56011
BX467899
BX387403
BM466011
BX467899
BM3410112
BM341018
BM3410115
BM3410115
              BM561588
BM806996
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/db_xref="taxon:9606"
/tjone="CSODIO40Y106"
/tissue type="placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Homo sapiens (human)
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1219 GAGGAAGAGGAGATCGGGAGCCCTGAGC 1204 CTCAGCCCCCTACAGAAGCTAAGCAGCA 1279 CTCAGCCCCCTACAGAAGCTAAGCAGCA 1324 TTGGACCGTCTGCTTGCCTCCCAGGGGA 1324 CGAGAGCGATGGTGCTTGCTCCCCAGGGGA 1324 CGAGAGCGATGGTGCTTAATGAAGACAG 1399 CGAGAGCGATGGTGCTAATGAAGACAG 1399 CGAGAGCGATGGTGCTAATGAAGACAG 1399 CGAGAGCGAATGATGAAGACAGGCA 1399 AACCATTGTCCCACAAAGAACTGGAGGCCA 1444 AACCATTGTCCCACAATG 1461 1519 AACCATTGTCCCACAATG 1536	EL SEDECS S	Shibata,K., Itoh,M., Aizawa,K Shibata,K., Itoh,M., Aizawa,K K Sono,H., Akiyama,J., Nishi,K. Kono,H., Akiyama,J., Nishi,K. Kono,H., Ishi,Y., Nakamura,S Yamamoto,R., Matsumoto,H., Sa Yamamoto,R., Inoue,K., Togawa Yoneda,Y., Ishikawa,T., Ozawa Okazaki,Y., Muramatsu,M., Ino RIKEN integrated sequence and sequencing pipeline with 384 Genome Res. 10 (11), 1757-177 Genome Res. 10 (11), 1757-177 ED 11076861 CE 4 (11), 1757-177 ED 1076861 RS THE KEN Genome Exploration FANTOM Consortium. Functional annotation of a functional phase I & II Team. Group Phase I & II Team. Analysis of the mouse transcraph
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awa,K., Nagaoka,S., Sasaki,N., Carninci,P., Ira,K., Kitsunai,T., Tashiro,H., Itoh,M., Ira,S., Hazama,M., Nishine,T., Harada,A., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Zawa,X., Tawa,M., Ohara,E., Watchiki,M., Tanaka,T., Matsuura,S., Kawai,J., Inoue,Y., Kira,A. and Hayashizaki,Y., analysis (RISA) system--384-format analysis (RISA) system--384-format 1-171 (2000)
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S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horit, F., Imchari, K., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsaro, N., Okazaki, Y., Saito, R., Saito, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shihagawa, A., Shiraki, T., Sogabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, Pax:81-45-503-9222, Pax:81-45-503-9216)
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URL:http://genome.gsc.riken.jp/
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Location/Qualifiers
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                                                                                                                                                                       prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
1. .2056
                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/64"
/db_xref="PANTOM_DB:2400004116"
/db_xref="taxon:10090"
/clone="2400004116"
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramateu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (202)
6 (bases 1 to 2056)
                                                                                                                                              AK075922 2056 bp mRNA linear HTC 03-APR-2004 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2400004116 product:kinesin superfamily protein KIF22, full
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-560 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                          was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7766.r
                                                                                                                                                                                                                       /tissue type="Piacenta COT 25-NORMALIZED"
/clone lib="Homo sapiens Placenta COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer live prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                            For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI009CE01QP1&c=7766. Location/Qualifiers
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the Not I and EcoR V sites of the procemalized. Library was constructed
                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1009YJ01"
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Best Local Similarity 96.9
Matches 1017; Conservative
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1. (bases 1 to 1124)

2. Li, W.B.; Gruber, C., Jessee, J. and Polayes, D.

3. Li, W.B.; Gruber, C., Jessee, J. and Polayes, D.

4. Full-length cDNA libraries and normalization

5. Loon Feb 15, 2001 this sequence version replaced gi:31267547.

6. Contact: Genoscope

6. Genoscope - Centre National de Sequencage

7. Rep. 191066 EWRY cedex - France

8. France

8. Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned
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AL545712.3 GI:45746191
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                                       CAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCAA
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BX337353 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI040YI06 5-PRIME, mRNA sequence.
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GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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1 (bases 1 to 1027)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
Unpublished (2001)
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0DI041AE07QP1&c=7766.r.
hctp://www.genoscope.cns.fr/cdna?8=CS0DI041AE07QP1&c=7766.r.
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Pred. No. 1.2e-248;
3; Mismatches 0;
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llarity 99.6%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1031)

S NIH-WGC http://mgc.noi.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bisocience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1948 row! 1 column: 06

High quality sequence stop: 679.
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_6702754 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5454101
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                                                                                                                                                                                           Liw B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Upublished (2001)
On May 2, 2003 this sequence version replaced gi:30337600.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRAIL: seqret@genoscope.cns.fr, Web: www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                               Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Primates,
1 (bases 1 to 1032)
   GI:46272059
                                                            Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1083)

25 Li, W.B., Gruber.C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

10 Neb 15, 2001 this sequence version replaced gi:31283903.

11 Unpublished (2001)

12 On Feb 15, 2001 this sequence version replaced gi:31283903.

13 Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Email: squee@genoscope.cns.fr, Web : www.genoscope.cns.fr
Enail: and EcoRV sites of the provSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 7766.r

For more information about this cluster, see
For more information about this cluster; see
http://www.genoscope.cns.fr/cdna?s=CSODG005CF06QP1&c=7766.r.
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/mol_type="mRNA"
/db xref="taxon:960s"
/db xref="taxon:960s"
/clone="CSDGGOSYLI1"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/coll_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/clone_lib="Tomo sapiens B CELLS (RAMOS CELL LINE)"
/clone_lib="Tomo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                         AL559772 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CSODG005YL11 5-PRIME, mRNA sequence.
AL559772 AL559772 GI:46185144
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62.3%; Score 912.8; DB 1;
larity 96.1%; Pred. No. 2.5e-232;
Conservative 13; Mismatches 21;
                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                            Homo sapiens
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Best Local Simi
Matches 942;
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// organism="Homo sapiens"
// organism="mRNA"
// organism= traxon:9606"
// orlone= traxon:9600"
// clone= trype="NEUROBIASTOWA"
// clone= trype="Homo sapiens NEUROBIASTOWA"
// note="type="Homo sapiens NEUROBIASTOWA"
// note="voctor: powySpORT" 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCWVSPORT 6 vector.
Library was not normalized."
       cloned
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end enriched, double-strand cDNA was digested with Not I and clone into the Not I and ECGRV sites of the pCNVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, division of Invitrogen.

This sequence belongs to sequence cluster 7766.r

For more information about this cluster, see http://www.genoscope.nns.fr/cdna?s=CSODA009CB01QP1&c=7766.r.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                               61.3%; Score 897; DB 1; I
larity 98.5%; Pred. No. 4.1e-228;
Conservative 3; Mismatches 8;
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Matches 923; Conserv
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Genoscope - Centre National de Sequencage
BPP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL518361 Anno sapiens 1016 bp mRNA linear EST 23-MAR-2004 AL518361 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone CSODA009YD01 5-PRIME, mRNA sequence.
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                                                                                                     CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA
                                                                                                                                                                                                    CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA
                                                                                                                                                                                                                                                  GACCTCCTGGACCCTGCTTCGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
                                                                                                                                                                                                                                                                           GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
                                                                                                                                                                                                                                                                                                                       CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC
                                                                                                                                                                                                                                                                                                                                           CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC
                                                                                                                                                                                                                                                                                                                                                                                            CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGC
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                                                     TATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCCAGCCCAGAGCAACCTGGG
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Vall-length CDNA libraries and normalization Unpublished (2011)
On Feb 13, 2001 this sequence version replaced gi:30536600
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BX363358 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens cDNA clone CSODK012YE23 5-PRIME, mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Contact: Robert Strausberg, Ph.D.
Email: cgapber: Garausberg, Ph.D.
Email: cgapber: Garauspergenent: Dr. Daniel Movicar, DBS/NCI
Tissue Procurement: Dr. Daniel Movicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayd by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://inage.llnl.gov
Plate: LLCM2116 row: b column: 13
High quality sequence stop: 690.
Liccation/Qualifiers
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Pred. No. 2.5e-224;
0; Mismatches 23; Indels 13;
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BCORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ053671 971 bp mRNA linear EST 29-MAR-2002
AGENCOURT 7025845 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935518
5., mRNA sequence.
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NH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
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         CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA
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                                                                         CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2123 row; g column: 07
High quality sequence stop: 660.
Location/Qualifiers
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/organism="Homo sapiens"
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1 (bases 1 to 959)

2 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

3 Full-length cDNA libraries and normalization

LU Unpublished (201)

On May 5, 2003 this sequence version replaced gi:30368690.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NoI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was a grand other was normalized with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .959
/organism="HOmo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOBK012YE23"
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/cell_line="HELA"
/clone_lib="HOmo sapiens HELA CELLS COT 25-NORMALIZED"
/clone_lib="HOmo sapiens HELA CELLS COT 25-NORMALIZED"
/nore="tax friand cDNA was primed with a NorI-oligo (dr)
primer. Five prime end enriched, double-strand cDNA was
digested with Nor I and cloned into the Nor I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 7.5e-224;
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                           GI:46287820
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 9106 EVRY CEDEX
BP 191 9106
                                                                                                                    958 bp mRNA linear EST 08-APR-2004
BX354166 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CSODC015YH04 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="NETROBLASTOMA COT 25-NORMALIZED"
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/clone_lib: strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases I to 958)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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99.9%;
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Best Local Similarity 99.9
Matches 885; Conservative
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Location/Qualifiers 11538 /organism="unknown" /mol_type="unassigned DNA"	Query Match 99.8%; Score 1112.4; DB 6; Length 1538; Best Local Similarity 99.9%; Pred. No. 1.3e-277; Matches 1113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Oy 1 ATGCAGCGGGGCTCGACGCAGCAGGCAACGCGAGATGGCGCAGCTTCAGCGG 60	Oy 61 CGGCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCAC 120	Qy 121 CTCCAGCTCGCGTAAGGGTGGCTGTGCGACTGCGGCCATTTGTGGATGGA	Oy 181 CAAGTGATCCCCCTGTGTGCGGGGCATGGACGCTGCTCTAGAGATTGCTAACTGGA 240	Oy 241 GGAACCACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTC 300	Oy 301 AGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGA 360	Oy 361 ATGCCAGTGTGCTTAGGACCCACAGGAGGAACACGCACACAATGCTGGGCA 420	Oy 421 GCCCAGAGCAACCTGGGGTGATCCCGCGGGCTCTCATGGACTCCTGCAGGTCACAAGGG 480	Qy 481 AGGAGGGTGCCGAGGCCATGGGCCTTTCTGTCACCATGTCTTACCTAGAGATCT 540	Oy 541 ACCAGAGAAGGTATTAGACCTCCTGGACCTGCTTCGGGAGACCTCGTAATCCGAGAAG 600	Oy 601 ACTGCCGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTG 660	Qy 661 ATTTGAGGGGACTTCCTGCCAGTGGAAATCGGACTGTAGGAGCCACCGGGTCA 720	Qy 721 ACCAGCGCTCCTCCCGCAGTCATGCTGTCCTGGTCAAGGTGGACCAGCGGGAACGTT 780 Db 721 ACCAGCGCTCCTCCCGCAGTCATGCTGTGCTCCTGGTCCAAGGTGGACCAGCGGGAACGTT 780	Oy 781 TGGCCCATTTGGCCAGAGGGAAAACTCTACCTGATTGGCTGGGTCAGAGG 840 1	QY 841 ACAACCGGGGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACCCT 900 DD 841 ACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCATCAACCATCAACCT 900	Qy 901 CCCTGTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTC	
Db 241 GGAACCACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTC 300 Qy 301 AGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGA 360	QY 361 ATGCCAGTGTGCTTGCCTATGGACCCACAGGAGCTGGGAAGACGCACAATGCTGGGCA 420	Oy 421 GCCCAGAGCAACCTGGGGTGATCCCGGGGGCTCTCATGGACCTCCTGCAGCTCACAAGGG 480 bb 421 GCCCAGAGCAACCTGGGGTGATCCCGCGGGTTCTCATGGACCTCCTGCAGCTCACAAGGG 480	Qy 481 AGGAGGGGCGAGGGCCATGGGCCCTTTCTGTCCCATGTCTTACCTAGAGATCT 540 Db 481 AGGAGGGTGCCGAGGCCGTCCTTCTGTCACCATGTCTTACCTAGAGATCT 540	OY 541 ACCAGAGAAGTATTAGACCTCCTGGACCGCGGAGACCTGGTAATCCGAGAAG 600 bb 541 ACCAGGAGAAGGTATTAGACCTCCTGGACCTGCTTCGGGAGACCTGGTAATCCGAGAAG 600	Oy 601 ACTGCCGGGGGAATATCCTGATTCCGGGTCTCTCCCGAAAGCCCATCAGTAGCTTTGCTG 660	Oy 661 ATTTTGAGGGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCA 720	Qy 721 ACCAGGGTCCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACGGGGAAGGTT 780 Db 721 ACCAGGGCTCCTCCCGCAGTCATGCTGTGCTCTGGTCAAGGTGGACGAGGGGAAGGTT 780	Qy 781 IGGCCCATTICGCCAGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGG 840 	Qy 841 ACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGAG	Oy 901 CCCTGTTTGTCCTGGGCAAAGTGGTAGATGGGCTGAATCAGGGCCTCCCTGGTGTACCTT 960	Qy 961 ATCGGGACAGCACACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA 1020	Qy 1021 TCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCA 1080	Oy 1081 ACTTTGCTGCCAGGTCCAAGAGTGATGA 1115 Db 1081 ACTTTGCTGCCAGGTCCAAGGAGGTGATCAATTGA 1115		LOCUS AR210053 1538 bp DNA linear PAT 20-JUN-2002 DEFINITION SEQUENCE 3 from patent US 6387644. ACCESSION AR210053 VERSION AR210053.1 GI:21512183	Unknown. Unclassified.	REFERENCE 1 (bases 1 to 1538) AUTHORS Beraud, C. TITLE Motor proteins and methods for their use	Par

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Pred. No. 2.6e-276;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 1108; Conservative
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Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Koundinya, M., Maphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

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Linder, Mark-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Bach CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been the Sall and HindlII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindlII site to maintain reading frame.

Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini; Hominidae, Homo.
1 (Dases 1 to 1998)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,W., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M., and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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SEBDRRTYGBKGLRLKESGAINTSLEVLGKVVDALNGSLPRVPYRDSKLTRLLQDSLG
GSABISILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPVKLSQKE
LLGPPEAKRARGPEEBESIGSPEPMAAPASASGOKLSPLOKLSSMDPANLERLJSLDRIL
ASQGSQGAPILSTPKRERMVLMKTVEEKDLEIERLKKVQKELEAKMLAQKAEEKENHC
                                                                                                  TCCTTATTGCCAACATTGCCCCTGAGACGCTTCTACCTAGACACAGTCTCCGCACTCA 1080
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VAVRLRPPYOGTAGASDPCYRGMDSCSLEIANWRNHQETLKYQPDAFYGERGTQQD
IYAGSVQPILRHLLEGANASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTRE
EGABGRPWALSVTMSYLEIYQEKVLDILDPASGDLVIREDGRGNILIPGLSQKRPISSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="BD Creator(TM) CDS Library derived from MGC collection"
                                              ATGGGACAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA
                                                                                                                                                                                                                                                                                                                          1998 bp mRNA linear
Homo sapiens kinesin-like 4 mRNA, complete cds.
BT007259
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/note="Vector: pDNR-Dual"
                                                                                                                                                                                        ACTITGCTGCCAGGTCCAAGGAGGTGATCAATTG 1114
                                                                                                                                                                                                          ACTITICTICCAGGICCAAGGAGGIGATCAATCG 1114
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protein_id="AAP35923.1"
db_xref="GI:30583357"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH00245X1.0"
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Homo sapiens (human)
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TITLE JOURNAL

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PEATURES

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AUTHORS JOURNAL

REFERENCE AUTHORS

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PTWLRPLSHRTVTGAKPLKKAVVMPLQLIQEQAASPNAEIHILKNKGRKRKLESLDAL
EPBEKAEDCWELQISPELLAHGRQKILDLINEGSARDLRSLQRIGPKKAQLIVGWREL
HGPPSQVEDLERVEGITGKQMESFLKANILGLAAGQRCGASL"
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                                                                                            Score 1107.4; DB 12
Pred. No. 2.6e-276;
0; Mismatches 1;
                                                                                                99.3%;
                                                                                                Query Match 99.3
Best Local Similarity 99.9
Matches 1108; Conservative
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This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pONR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence, 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
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RVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIAMWNHQETLKYQPDAFYGERSTQQD
RYAGSVQPILLHELLEGQMSAVLAXQPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTRE
EGABGREPWALSVYMSYLEIYOBKYLDLUPASGDLVIREDCRGNILIPGLSQKPISSF
ADFERHPLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLA
GSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALDANGALPFVPRDSKTATLLQDSLG
GSEDRRTGNKGLRLKESGAINTSLFVLGKVVDALDVORLPRYPRDSKTATLLQDSLG
GSABSILLIANIAPERRFYLDTVSALNPAARSKEVINRPFTNESLQPPRLSQKI
LLGPPBAKRARGPEEBEIGSPERMAAPASASQKLSPLOKLSSRDPAAMLERLLSDRIL
ASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKYKQKELEARMLAQKABEKENHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
2 (bases 1 to 1998)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Kondinya.M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.
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Synthetic construct Homo sapiens kinesin-like 4 mRNA, partial cds.
                                                                                ATTGCCAACATTGCCCCTGAGAGGCGCTTCTACCTAGACACAGTCTCCGCCACTCAACTTT 1085
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         GACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTT
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/product="Homo sapiens kinesin-like
/protein id="AM>36560.1"
/db_xref="GI:30584615"
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note="Mutations: 1997:Stop->Leu"
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/note="Vector: pDNR-Dual"
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/mol_type="mRNA"
/db_xref="taxon:32630"
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Homo sapiens mRNA for kinesin-like DNA binding protein, complete
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Direct Submission.

Direct Submission.

Submitted (03-SEP-1998) Noriko Tokai-Nishizumi, The University of Submitted (03-SEP-1998) Noriko Tokai-Nishizumi, The University of Tokyo, The Institute of Medical Science, Department of Oncology; 4-6-1 Shirokanedmi, Minato-ku, Tokyo 108-8639, Japan (B-mail:tokai@hdg.ims.u-tokyo.ac.jp, Tel:03-5449-5302, Pax:03-5449-5413)

D38751:Submitted (02-Nov-1994)
Sequence updated (25-Peb-1999).
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                   GAGCGGCACTTCCTGCCAGCCAGTCGAATCGGACTGTAGGAGCCACCCGGCTCAACCAG
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                                 GAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAGACTGC
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AB017430.2 GI:4519442
Kid; kinesin-like DNA binding protein; kinesin family.
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1024 ATTGCCAACATGCCCCTGAGAGACGCTTCTACCTAGACAGTCTCGGGACTGTGAACTTT
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Sequence 34 from patent US 6544766.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="pBskid"
/cell_type="breast cancer'
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                                                                                                                                                                                                                             /product="kinesin-like DN
/protein_id="BAA33019.2"
/db_xref="G1:4519443"
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                                                                                                                                                                                                                                                                      Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Web site: http://www.nisc.nih.gov/
Achter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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McDowell, J., Peargoon, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogf, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 62 Row: 1 Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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                    Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Pred. No. 2.6e-276;
0; Mismatches 1; Indels 0;
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                                                                                                  USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
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Best Local Similarity 99.9%;
Matches 1108; Conservative 0
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AUTHORS
TITLE
JOURNAL
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DEFINITION

RESULT 8 BC004352

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ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L. UORBERG N. L. Peingold, E. A., Grouse, L. H., Derge, J. G., Klausberg, R. L., Peingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. L., Colling, F. S., Wagner, L., Schender, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buet, M. H., Monze, T. Mars, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T. L., Schetz, T. E., Brownstein, M. J., Ugdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Morkernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Backy, K. G., Hale, S., Garcia, A. M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Butterfield, Y. S., Krzywinski, M. I., Skalsa, U., Schevich, D. E., Schein, J. B., Schein, J. B., Schein, J. B., Schein, J. B., Schein, J. S., Krzywinski, M. I., Skalsa, U., Smailus, D. E., Schein, J. B., M. A., Schein, J. B., J. M. Salsa, J. and Marra, M. A., Schein, J. B., J. Schein, J. Schein, J. Schein, J. B., Schein, J. Schei
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Contact: MGC help desk
Contact: MGC help desk
Email.cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canda
info@boggo.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Reatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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This clone was elected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817.
Location/Qualifiers
                                                                                                                                                                                                                          2134 bp mRNA linear PRI 29-JUN-2004 nily member 22, mRNA (cDNA clone MGC:1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo.
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2477932
   human and mouse cDNA sequences
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IMAGE:3535435), complete cds.
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REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

PUBMED

JOURNAL

TITLE

/organism="Homo sapiens" /mol_type="mRNA"

source

FEATURES

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                                                                                         OBP-1, OBP-2, KNSL4"
colone="MGC:1573 IMAGE:3535435"
/tissue type="Lung, small cell carcinoma"
/clone_lib="NIH_MGC_7"
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                                                                                                                                                                                                                                                                                                                                                                                                                           99.3%; Score 1107.4; DB 9.99.9%; Pred. No. 2.6e-276; iive 0; Mismatches 1;
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U-U H-H (C-C 4-4 C-C)-C 4-4 L-L 4-4 C-C

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Mus musculus (house mouse)
Mus musculus
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Pred. No. 1.2e-257;
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/organism="unknown"
/mol_type="unassigned DNA"
                         1 (bases 1 to 1464)
Beraud, C.
Motor proteins and methods for their
Patent: US 6387644-A 7 14-MAY-2002;
Location/Qualifiers
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Best Local Similarity 99.9%;
Matches 1036; Conservative
Unknown.
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Mus musculus clone RP24-158A6, WORKING DRAFT SEQUENCE, 4 unordered
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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-158A6
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bogullavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Hotton, L., Hulme, W., Iliev, I., Johnson, R.,
                                                                                                                                                                                              661 TGACTTCGAGCACTTCCTTCCAGCCAGTAGAAATCGAGCTGTAGGAGCCACCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               721 TAACCAGGGCTCTTCCCGTAGTCACGCAGTGCTCTTGGTCAAGGTAGATCAGCGTGAACG
         TTTGGCCCCATTTCGCCAGCGAGAGGGAAACTCTACCTGATTGACTTGGCTGGGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           959 TTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAG
                                                                                                                           GGAAGAGAGTGCTGAGGGACGCCATGGGACGTTTCTGTTGCTATGTCCTATTTAGAGAT
                                                                                                                                                                  CTACCAGGAGAAGGTATTAGACCTCCTGGACCTGCTTCGGGAGACCTGGTAATCCGAGA
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                                                                                                                                                                                                                                                           AGACTGCCGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGC
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AC101919 4 GI:28951338
HTG: HTGS_PHASE1; HTGS_DRAFT.
MMUS musculus (house mouse)
Mus musculus
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TITLE
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: m Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21704181. Location/Qualifiers
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/clone_lib="NCI_CGAP_Mam6"
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ILIANIAPERREYQDTISALNETARSKEVINNEPTNUSLQPHALAPVKLSQKELLGPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonym: Kid"
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                                                                                                                                                                                                                                                                                                              Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McBwan, P., McKernan, K., McPheters, R., Meldrim, J.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Sosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Lavers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 150741; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L17745
Center clone name: 158_A_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
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COMMENT

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65428 CAGAATGCCAGTGTACTTGCCTATGGACCGACTGGGGAGGAGGA--CACACAATGTTG 65371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65668 CTGCTTCTAGCTGGAGTAAGGGTGGCTATATAATTGTGCCTGTTTGTGGATGAAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55310 AGGGAAGAATGCTGAGGCTGGCCATGGGACATTTCTGTTGCTTTGTGCTATTTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAGCCCAGAGCAACCTGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 AGGGAGGAGGGTGCCGAGGCCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGCGGCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGT
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    contig of 33517 bp in length 100 bp 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
of 33517 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.1%; Score 681.4; DB 2;
79.7%; Pred. No. 9e-166;
iive 0; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                               1. .151041
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector side:left"
33618. .42736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone end:SP6
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                                                                                                                                                                                                                 84494:
151041:
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42836:
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Best Local Similarity 79.73
Matches 844; Conservative
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33618
42737
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84395
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Direct Submission

Livert Submission

Livert Submission

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Streen, B. Nusbaum, C., Lander, B., Abouelleil, A., Allen, N.,

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

Bloom, T., Boguslavkiy, L., Boukhgalter, B., Canarata, J., Chang, J.,

Choepel, Y., Collymore, A., Cook, P., Cook, P., Corum, B.,

Brickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,

Galagan, J., Gardyna, S., Graham, L., Grand-Pleire, N., Hafez, N.,

Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I.,

Johnson, R., Lindblad-Toh, K., Liu, G., Liu, X., Lul, A., Mabbitt, R.,

MacLean, C., Macdonald, P., Maning, J., Matthews, C.,

Maczerthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,

Murphy, T., Naylor, J., Wquyen, C., Nquyen, T., Mlenga, V.,

Phunkhang, P., Pierre, N., Rachupka, B., Schauer, S., Schupback, R.,

Seaman, S., Severy, P., Somith, C., Schauer, S., Schupback, R.,

Scoman, S., Savery, P., Somith, C., Schauer, S., Schupback, J.,

Scoman, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,

Vo, A., Wilson, B., Wu, X., Wyman, D., Young, C., Zainoun, J., Zembek, L.,

Direct Submission
                                 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgaller, B., Camarata, J., Chang, J., Choepel, Y., Cook, A., Cook, P., Corum, B., DeArellano, K., Cook, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagez, N., Hagopian, D., Hagos, B., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Peterson, K., Phunkhang, P., Pierre, N., Schuber, J., Schuber, C., Schuber, J., Schuber, J., Schube, M., Schauer, S., Schuber, R., Seaer, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbe, M., Vassiller, H., Venkataraman, V. S., Viel, K., Tavers, M., Wann, D., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 23, 2004 this sequence version replaced gi:45504330. All repeats were using the sung RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-24 Male Mouse BAC" 1. .1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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           REPERENCE
                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   953 TGTACCTTATCGGGACAGCAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCACC 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1013 CCACAGTATCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTC 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC101752 164759 bp DNA linear ROD 23-APR-2004
Mus musculus chromosome 1, clone RP24-344C18, complete sequence.
AC101752
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                                                                                                                                                                                                                                                                                                                                                                                                                   892
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 164759)
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                                                                                                                                                                                                                                                                                                             CGTTTGGCCCCATTTCGCCAGCGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54830 TATACCATACCAGGACAGGCTCACTCGTCGTTGCAAGACTCTCTGAGAGGCTCAGC
                                                                                                                 CTCAACCAGCGCTCCTCCCGCAGTCATGCTGTTCCTGGTCAAGGTGGACCAGCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                        837 GAGGACAACC----GGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64710 AGCATTAAACTTCACTGCTAGGTCCAAGGAGGTGATTAA 64672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1073 CGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAA 1111
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Mus musculus chromosome 1, clone RP24-344C18
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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/rpt family="Li MM"
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/rpt_family="(TTC)n"
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MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrin,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Riee,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Scaman,S., Severy,P., Smith,C., Spence,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Teefaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vol,M., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Direct Submission
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
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78.1%; Pred. No. 1e-158;
...rive 0; Mismatches 223; Indels
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------ Project Information
Center project name: L17732
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/clone_lib="RPCI-24 Male Mouse BAC"
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Web site: http://www-seg.wi.mit.edu

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          953 TGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGC 1012
                                                                                                                                                                                                                                                                                                                                                                            1013 CCACAGTATCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTC 1072
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297639 bp DNA linear HTG 18-JUN-2004
Mus musculus chromosome 1 clone RP24-275J1 map 1, *** SEQUENCING IN
PROGRESS ***, 8 unordered pieces.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 297639)
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                                                                                                                 145122 AGCATTAAACTTCACTGCTAGGTCCAAGGAGGTGATTAA 145084
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HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
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177 GGAGCAAGTGATCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTTAGAGTTGCTAAC 1088 GAAGCGAAGGACCCCTGTGTACGAGCCATAGACGCTGCTCTTTGAAGTGGCTAAC 237 TGGAGGAACCACCCTGTGTACGAGCCATAGACGCTGCTCTTTGAAGTGGCTAAC 237 TGGAGGAACTACCAGGAGCTTCAAATATCAGTTTGATGCCTTCCATGGGGAAGGGG 297 ACTCAGCAGGACATCTATGCAGGTTCAATGCCTTCCATGGAGAGAGGG 297 ACTCAGCAGGACATCTATGCAGGTTCAGTGCCCATCCTTGAAGGACTTGCTGGAAGGG 357 CAGAATGCCAGTGTATGATCAGTACAGCCCATACTAAGGAACTTGCTGGAAGGG 357 CAGAATGCCAGTGTTCTTGATGACCCATACTAAGGAACTTGCTGGAAGGG 357 CAGAATGCCAGTGTTCTTTGATAGGACCCATACTAAGGAACTGCTGGAAGGG 358 ACTCAGCAGTGTACTTGCTATGGACCGATGGGAGGAAGAGACGCCATAGTTGTTGTTAGTACTGGAGCCGATGGAGGAAGACGCCATAGTTGTTAGTACTTGTAGGACCGATGCTGGAGCGAGGAAGACCCAGAGTGTTGTTAGTACTTAGTACTGAAGGGAAGACAGAGACAGAGACGAGAGACAGAC	537 ATCTACCAGAGAAATGCTTAGACCTCCTGGACATTTCTGTTGCTTTGTGCTTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTCCGAAATGCTTCTTGGAAACTGTTCCGAAATGCTTTTGTTCTTAGATTCCTGAATGCTTTTTGTTGTTCCTTAAATGCTTTTTGTTCTTAAATGCTTTTTGTTGTTTTGTTTTTTTT	### ### ##############################
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AC102127 196674 bp DNA linear ROD 01-MAY-2004 Mus musculus chromosome 1, clone RP23-202A19, complete sequence.

Mus musculus (house mouse)

GI:46931440

AC102127 AC102127.11 HTG.

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        Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R. Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasalilev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Direct Submission

L. Submitted (01-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 1, 2004 this sequence version replaced gi:46358225.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
Center: Project Information
Center project name: L18071
Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 AGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGG 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 TGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGGGGAAGTGATCCCCCTGTGTGCG
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| Cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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	Description	sence 7, Appli	Sequence 3, Appli	sequence 102, App	Sequence 288, App	nence 5, Appli	lence 1, Appli	Sequence 131, App	lence 1937, Ap	Sequence 1180, Ap	lence 31705, A	sence 1177, Ap	Jence 10603, A
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Query Match
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Sequence 24303, A Sequence 249, App Sequence 305, App Sequence 105, App Sequence 160, App Sequence 6, App Sequence 6, App Sequence 2129, App Sequence 2129, App Sequence 313, App Sequence 313, App Sequence 313, App Sequence 314, App Sequence 23, App Sequence 215, App Sequence 21668, A Sequence 21668, A Sequence 21668, A Sequence 21668, A Sequence 21668, App Sequence 21668, App Sequence 21668, App Sequence 2161, App Sequence 2163, App Sequence 2164,	N.
US-10-029-386-24303 US-10-20-386-24303 US-10-20-26-301 US-10-20-26-301 US-09-883-096-1 US-10-883-096-1 US-10-437-963-1460 US-10-437-963-1460 US-10-425-114-25129 US-10-425-115-148256 US-10-425-115-148256 US-10-311-642-1 US-10-311-642-1 US-10-311-642-1 US-10-311-642-1 US-10-311-642-1 US-10-311-642-1 US-10-311-625-32 US-10-311-625-32 US-10-076-555-32 US-10-076-555-32 US-10-076-555-32 US-10-076-555-32 US-10-076-555-32 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	ALIGNMENTS ULT 1 10-797-893-7 equence 7, Application US/10797893 ublication No. US20040142397A1 ENREAL INFORMATION: ENREAL INFORMATION: ENERGY OF INVENTION: TITLE OF INVENTION: their use FILE REFERENCE: 1044 CURRENT APPLICATION NUMBER: US/10/797,893 CURRENT APLICATION NUMBER: US/09/724,224 PRIOR FILING DATE: 2000-11-28 PRIOR APPLICATION NUMBER: 09/597,292 PRIOR FILING DATE: 2000-11-28 PRIOR FILING DATE: 2000-11-28 ENGINE APPLICATION NUMBER: 09/597,292 PRIOR FILING DATE: 2000-11-28 PRIOR FILING DATE: 2000-11-28 ENGINE APPLICATION NUMBER: 09/597,292 PRIOR FILING DATE: 2000-11-28
232 15 33.095 16 4108 9 616.50 16 16.50	RESULT 1 US-10-797-893-7 Sequence 7, Application US/107978; Publication No. US20040142397A1 GENERAL INFORMATION: APPLICANT: Beraud, Christophe TITLE OF INVENTION: Novel motor 1 TITLE OF INVENTION: their use FILE REFERENCE: 1044 CURRENT APPLICATION NUMBER: US/10 CURRENT PELING DATE: 2000-06-20 PRIOR FILING DATE: 2000-10-28 PRIOR FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Vering NUMBER: OF SEQ ID NO 7 LENGTH: 1464 TYPE: DNA ORGANISM: Human US-10-797-893-7
1111 100000000000000000000000000000000	Application No. US2004(ORMATION: ORMATION: WENTION: WENTION: UNGENTION: ULING DATE: LICATION NUMR NG DATE: 200 ICATION NUMR HUMAN 464
4 0 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	SULT 1 -10-797-893-7 Bequence 7, Applicati Bublication No. US200 GENERAL INFORMATION: APPLICANT: Beraud, TITLE OF INVENTION: TITLE OF INVENTION: TITLE REFERENCE: 1044 CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION FRIOR APPLICATION NU PRIOR APPLICATION NU PRIOR FILING DATE: 2 PRIOR FILING DATE: 2 RIOR FILING DATE: 2 RIOR FILING DATE: 2 RIOR FILING DATE: 2 ROSTWARE: FastSEQ fo LENGTH: 1464 TYPE: DNA ORGANISM: Human -10-797-893-7
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Sequence 102, Application US/10334143
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| Publication No. US20040009549A1
| GENERAL INFORMATION:
| APPLICANT: SUDARSANAM, SUCHA
| APPLICANT: SUDARSANAM, SUCHA
| TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
| TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
| TITLE OF INVENTION: METHOD FOR DETECTION BETHOD
| FILE REFERENCE: 038602/1543
| CURRENT FILING DATE: 2002-12-31
| PRIOR APPLICATION NUMBER: 60/343,169
| PRIOR APPLICATION NUMBER: 60/343,169
| PRIOR PEDIATOR DATE: 2001-12-31
| SEQUENCE FILING DATE: 2007
| SEQUENCE FILING DATE: 2007
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ORGANISM: Homo sapiens
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Best Local Similarity 99.4%;
Matches 1450; Conservative
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LENGTH: 2104
TYPE: DNA
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US-09-925-300-288
US-09-925-300-288

Squence 288, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO1
CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT APPLICATION NUMBER: US/09/925,300

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Novel motor proteins and met
TITLE OF INVENTION: their use
FILE REPERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/09/724,224
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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Publication No. US20040142397A1
GENERAL INFORMATION:
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Best Local Similarity
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; TYPE: DNA
; ORGANISM: Human
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                                                                                                             798 CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC
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Pred. No. 2.3e-138;
0; Mismatches 0; Indels
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APPLICANT: Mohamath, Raodoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.556
CURRENT APPLICATION UNMERE: US/09/960,253
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FREUSED FOR Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 131, Application US/09960253; Patent No. US20020123619A1; GENERAL INFORMATION:
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Best Local Similarity 99.8%;
Matches 491; Conservative C
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ORGANISM: Homo sapiens
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                                                            Sequence 1, Application US/1079893
; Publication No. US2004014297A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENDTH: 1115
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Best Local Similarity
Matches 1036; Conserv
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US-10-797-893-1
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121 CCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAGC 180
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                                                                       181 GCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGCCCCTCTGTTGA
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 5.29452001122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR APPLICATION NUMBER: US 09/798,586
FRIOR FILING DATE: 2001-10-3-02
NUMBER OF SEQ ID NOS: 2059
NUMBER OF SEQ ID NOS: 2059
SEQ ID NO 1180
LENGTH: 24525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%; Score 365; DB 13; 73.8%; Pred. No. 5.1e-102; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                            1433 AGGAAAAGGAGAACCATTGTCCCACA 1458
                                                                                                                                                                                                                                                                               361 AGGAAAAGGAGAACCATTGTCCCACA 386
                                                                                                                                                                                                                                                                                                                                                                                        sequence 1180, Application US/10087192; Publication No. US20020182586A1
GENERAL INFORMATION: APPLICANT: MOTTIS, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 73.8
Matches 597; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1180
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                                                                                                                                                                                1073 CCTTGGGACCTGTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAG 1132
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                                                                                                                      360 GGGGCCCCTCTGTTGAGTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGA
                                                                                       GGGGCCCCTCTGTTGAGTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGA
                                                                                                                                                             1 CGTTGCTGTCGGTTAAGCTGTCTCAGAAGAAGAATTGCTTGGTCCACCAGAGGGCAAAGAGAG
                                                300 cccesccarscreaaccccrcrcascrreaacccrcrecrrecrrecrrecrreccasesca
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APPLICANT: Leshkowitz, Dena
APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
PILE REFERENCE: 1624.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 376.4; DB 10
Pred. No. 3.3e-106;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FABELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Becobedo, Jaime
Innis, Michael A.
Garcia, Pablo Dominiguez
Sudduth-Klinger, Julie
Reinhard, Christoph
Giese, Klaus
Randazzo, Filippo
Kennedy, Giulia C.
Pot, David
Kassam, Altaf
Lamson, George
Drmanac, Radoje
Crkvenjakov, Radomir
Dickson, Mark
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Publication No. US20030044783A1
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
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Best Local Similarity 98.4%;
Matches 380; Conservative (
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                                                                                                                                                                                                                                                            480 GTTGGCCCAGAA 491
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APPLICANT:
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APPLICANT:
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700 GAACGITIGGCCCCATITCGCCAGCGAGAGAAAACICTACCIGAITGACITGGCIGGG 759
                                                                                                                                                                                 GCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAGA 485
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                                                                                                           336 decardedecerriterereacerererraceradametraceaggagametrada 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 AGGIATIAGACCITCCTGGACCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGG
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CGGTGCCTGAGGAGCTGGCATTAC-ATCTCGATGCTTGGCAGCCCAGAGCAACCTGGGGT
                                                                                Gaps
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Sequence 1177, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Bragelhard, Eric K.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 52945200012.
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2001-02-02

PRIOR PLING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2009

SEQ ID NO 1177

LENGTH: 24291

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17.9%; Score 262.4; DB 1.3
Best Local Similarity 73.8%; Pred. No. 3.9e-70;
Matches 385; Conservative 0; Mismatches 61
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// LOCATION: (1)...(24291)

// OTHER INFORMATION: n = A,T,C or

US-10-087-192-1177
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ORGANISM: Mus musculus
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                                                                                                              2733 ATCAACACCTCCCTGTTTGTCTCGGCCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCT 2792
                                                                                                                                                                                                                    2793 CGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGTCAGGCCCACCTGTCTC 2852
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                GGGTCAGAGGACAACCGGCGCACAAGAGGGCCTTCGGCTAAAAGAGAGTGGAGCC 2732
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT RILING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/215,076
FRIOR PELICATION NUMBER: US/09/235,076
FRIOR PELICATION NUMBER: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOPTWARE: FastESEQ for Windows Version 3.0
SEQ ID NO 31705
LENGTH: 464
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Pred. No. 1.5e-71;
0; Mismatches 95;
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Publication No. US20030073623A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31705
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Best Local Similarity 77.6%;
Matches 333; Conservative (
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ORGANISM: Homo sapiens
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APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOUTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24303
LENGTH: 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO CHRIG.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: SWISSPROT HIT: 014807, EVALUE 5.00e-37
OTHER INFORMATION: BST HUMAN HIT: BR382882.1, EVALUE 1.00e-125
US-10-029-386-24303
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Pred. No. 1.2e-46;
0; Mismatches 379; Indels
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A01.06
CURRENT APPLICATION NUMBER: US/10/108,260A
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN NOT: 2.1
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Best Local Similarity 99.6
Matches 231; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Penn, David R.
APPLICANT: Pancel, David R.
TITLE OF INVENTION: HUAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERBOYER: ACOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                          3299 TCAGAGGACAACCGTCGCACAGGCAACCAGGGCATTCGGCTCAAAAGAGAGCGGAGCCATC 3358
                                                                                                                                                                                                                                                                                                                                                                                                    3359 AACACCICCITITGIACTGGGCAAAGTGGGATGCATTAAACCAGGGCCTCCCTCGC 3418
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: WT HIT: ABOL7334.1, EVALUE 0.000+00
OTHER INFORMATION: SWISSPROT HIT: Q14807, EVALUE 2.000-36
OTHER INFORMATION: EST_HÜMAN HIT: BF975048.1, EVALUE 1.000-126
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Publication No. US20030194704A1
GENERAL INFORMATION:
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Best Local Similarity 98.7
Matches 235; Conservative
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LENGTH: 531
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APPLICANT: Zerhueen, Bryan D.,
APPLICANT: Zerhueen, Bryan D.,
APPLICANT: Zerhueen, Bryan D.,
APPLICANT: Zhong, Mei
TITLE GP INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
CURRENT PILING DATE: 2002-11-04
FRIOR PELICATION NUMBER: 60/334,421
FRIOR FILING DATE: 2001-11-30
FRIOR FILING DATE: 2002-02-04
FRIOR FILING DATE: 2002-02-04
FRIOR PELICATION NUMBER: 60/360,148
FRIOR APPLICATION NUMBER: 60/360,148
FRIOR PELING DATE: 2002-02-03-13
FRIOR PELING DATE: 2002-03-03
FRIOR PELING DATE: 2002-03-03
FRIOR PELING DATE: 2002-03-03
FRIOR PELING DATE: 2002-03-04
FRIOR PELING DATE: 2002-03-04
FRIOR PELING DATE: 2002-03-04
FRIOR APPLICATION NUMBER: 60/334,409
FRIOR FILING DATE: 2002-03-13
FRIOR APPLICATION NUMBER: 60/334,409
FRIOR FILING DATE: 2002-03-13
FRIOR APPLICATION NUMBER: 60/334,409
FRIOR FILING DATE: 2002-03-13
FRIOR PILING DATE: 2001-11-28
FRIOR APPLICATION NUMBER: 60/334,409
FRIOR FILING DATE: 2001-11-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, Jr., Raymond J.
Vernet, Corine A.M.,
                                                                                                                                                                                                                                                                                                                                                                                     Padigaru, Muralidhara
                                                                                                   Malyankar, Uriel M.,
MacBougall, John R.,
Macse, Peter S.,
Miller, Charles E.,
Millet, Isabelle,
Ooi, Chean Eng,
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Rastelli, Luca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rieger, Daniel K.,
Rothenberg, Mark E
Shenoy, Suresh G.,
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ORGANISM: Homo sapiens
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                                                                                                                                                             430 TGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAGACCTC 489
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                                                                                                      Gaps
                                                                 Query Match
Best Local Similarity 54.1%; Pred. No. 1.3e-37;
Matches 395; Conservative 0; Mismatches 317; Indels 18;
; NAME/KEY: CDS
; LOCATION: (7)..(3351)
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Sequence 301, Application US/10287226 Publication No. US20040086875A1

RESULT 15 US-10-287-226-301

GENERAL INFORMATION:

APPLICANT: Ages, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Constance,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Edinger, Andrew,
APPLICANT: Blerman, Karen,
APPLICANT: Gangolli, Esha A.,
APPLICANT: Gargolli, Esha A.,
APPLICANT: Gargolli, Esha A.,
APPLICANT: Gargolli, Racen,
APPLICANT: Gargolli, Racen,
APPLICANT: Gargolli, Walerie,
APPLICANT: Gargolli, Walerie,

See File Wrapper or PALM

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963 GGTGACCGTGCGCCGCGCGCGGCCGAAAAACATCTTGCAGGAGGCGCAAGGCCGCCT 1022
                                                                                                                                                                                                                                                                              972 GAGACGCTTCTACCTAGACACACTCCGCACTCAACTTTGCTGCCAGGTCCAAGGAGGT 1031
                                                                                                                                                                                                                                                                                                                                        681 GGTCAAGGTGGACCAGCGGAACGTTT---GGCCCCATTTCGCCAGCGAGAGGGAAAACT 737
                                                                                                                                                         738 CTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCCACAGGGCCATTCG 797
                                                                                                                                                                                                                                      858 GCTGAATCAGG-----GCCTCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCT 911
                  783 ccredecraccredascrecesassasacrecrasses 842
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TTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGAATATCCTGATTCCGGGTCTCTC
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ATGGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTA
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         US-10-159-151-7

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US-09-162-373-2

US-09-162-373-2

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US-09-967-908A-9

US-09-967-908A-5

US-09-967-908A-1

US-10-159-151-9

US-10-159-151-13

US-09-967-908A-1

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US-09-632-344-3

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US-09-632-344-3

US-09-632-344-3
                                                                                                                                                                                                                                                                    Sequence 7. Application US/09724224
Facent No. 6387644
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor prot
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT PILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
FRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1464;
100.0%; Pred. No. 0;
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ORGANISM: Human
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Best Local Simi]
Matches 1464; (
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US-09-724-224-7
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US-09-724-224-7
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Sequence 34,
Sequence 5, A
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Sequence 7, P
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(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                  parent No. 6762043

| Sequence 77, Application US/10093317
| Patent No. 6762043
| CENERAL INFORMATION:
| APPLICANT: Beraud, Christophe
| TITLE OF INVENTION: No. 6762043e1 motor proteins and methods for TITLE OF INVENTION: No. 6762043e1 motor proteins and methods for TITLE OF INVENTION: Heir use
| FILE REFERENCE: 1044
| CURRENT APPLICATION NUMBER: 09/724,224
| PRIOR APPLICATION NUMBER: 09/724,224
| PRIOR PILING DATE: 2000-11-28
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 7
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Best Local Similarity 100
Matches 1464; Conservative
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; TYPE: DNA
; ORGANISM: Human
US-10-093-317-7
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                                                 Score 1461; DB
Pred. No. 0;
                                          99.8%; Scor.
100.0%; Pred. No. c,
... 0; Mismatches
                                                 Query Match 99.8
Best Local Similarity 100.
Matches 1461; Conservative
                Human
      ; TYPE: UNA
; ORGANISM: Ht
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; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644e1 motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT APPLICATION NUMBER: 09/597,292
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR PLING DATE: 2000-11-28
; SOFTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1538
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US-09-724-224-3
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	Query Match 99.6%; Score 1458; DB 4; Length 2097; Best Local Similarity 100.0%; Pred. No. 0; No. 0; Matches 1458; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 4 GGTCGCTGTCGGCTAAGCAAGTTGGAGCTACTCGTCGTCCACCTCGCGTAAGG 159 Db 100 GGTCGCTGTCGGCTAAGCAAGTTGGAGCTACTCGTCGTCCACCTCGCGGTAAGG 159 Qy 64 GTGGCTGTGCGACTGCGCAATTTGTGGATGGACGGGAGCAAGTGATCCCCCCTGT 219 Db 160 GTGGCTGTGCGACTGCGCCATTTGTGGATGGATCGCGGGAGCAAGTGATCCCCCCTGT 219 Qy 124 GTGCGGGCATGGACGCCATTTGTGGATGGATCGAAGTGATCCCCCAGGAGACT 279 Qy 124 GTGCGGGCATGGACGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACAGGAGACT 279 Qy 184 CTCAAATACCAGTTTGATGCTCTCTATGGGAGGAGTACTCAGCAGGAACTCTTATGC 339 Qy 244 GGTTCAGTGCAGCTCCTTCTATGGGAAGGGAGTACTCAGCAGGAATTGCTTGC

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US-10-093-317-5
US-10-093-317-5
; Sequence 5, Application US/10093317
; Sequence 5, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; TITLE OF INVENTION: Lheir use
; TITLE OF INVENTION: UMBER: US/10/093,317
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NOS: 8
; SEQ ID NO S: 8
; SEQ I
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US-10-093-317-5
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                                             US-09-74-24-24-5

1 Sequence 5, Application US/09724224

2 Patent No. 6387644

3 GENERAL INFORMATION:

3 APPLICANT: Bereaud, Christophe

3 TITLE OF INVENTION: No. 6387644el motor proteins and methods for

4 TITLE OF INVENTION: their use

5 TITLE OF INVENTION WIMBER: US/09/724,224

5 CURRENT FILING DATE: 2000-11-28

6 PRIOR APPLICATION NUMBER: 09/597,292

7 PRIOR APPLICATION NUMBER: 09/597,292

7 PRIOR FILING DATE: 2000-6-20

7 NUMBER OF SEQ ID NOS: 8

7 SOFTWARE: FastSEQ for Windows Version 4.0

7 SEQ ID NO 5

1 LENGTH: 1041

7 TYPE: DNA

7 OKGANISM: Human

US-09-724-224-5
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Pred. No. 8.8e-293;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 1039; Conservative
                                    -09-724-224-5
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Best Local S Matches 1036 78 64 138 124 198	258 CICLAAATACCAGTTTGATTTTTTTTTTTTTTTTTTTTTTTT	2 4 4 3 3 4 4 8 4 8 4 8 4 8 4 8 4 8 4 8 8 4 8	484 GACCTCCTGGACCCTGCTTCGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC 5	604 CTGCCAGCCAGTCGAAATCGGACTGTAGGACTTTGCTGATTTTGAGCGCTCCTCCGGCCACTTCGCGCTCCTCCGGCTCTTGCTGAATCGGAATCGGACTGTAGGAGCCACCGGCTCCAACCAGCGGCTCCTCCCGCCGGCTCCTCCGGCTCCTGGAATCGGACTGTAGGAGCCACCCGGGCTCAACCAGCGGCTCCTCCCGGCGAACGTTTGGCCCATTTCGCCCAGTTTGGCCCATTTCGCCCAACGTTTGGCCCATTTCGCCCAACGTTTGGCCCATTTCGCCCAACGTTTGGCCCAACGTTTGGCCCAATTTCGCCCAACGTTTGGCCCAACGTTTGGCCCAATTTCGCCCAACGTTTGGCCCCAATTTCGCCCAACGCGGGAAACGTTTGGCCCCAATTTCGCCCAACGCGGGAAACGTTTGGCCCCAATTTCGCCCCCCCC	724 CGAGAGGAAAACTCTACCTGATTGACTTGGCTCAGAGGACAACCGGCGCACAGGC 783		964 GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 1023
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Db 301 GCCTATGGACCCACAGGAGCTGGGAAGCACACATGCTGGGCCAGAGCCACCT 360	TTCTGCCGGCGGTCGAATCGGACTGTAGGACCCCCGGCTCCAACCGGCGCTCCTCC TTCTGCCGGCCAGTCGAAATCGGACTGTAGGACCCCCGGCGTCCAACCGGCGCTCCTCC TTCCTGCCAGCCAGTCGAAATCGGACTGTAGGACCCACCGGGCTCAACCAGCGGCTCCTCC TTCCTGCCAGCCAGTCGAAATCGGACTGTAGGCCGCCACTTTGCCCTCTCTCT		### ### ##############################	961 ATTGCCCTGAGAGACGCTTCTACCTAGACACTCTCGCACTCAACTTTGCTGCCAGG 1020	RESULT 8 US-09-724-224-1 ; Sequence 1, Application US/09724224 ; Patent No. 6387644 ; GENERAL INFORMATION: ; APPLICANT: Beraud, Christophe ; TITLE OF INVENTION: No. 6387644el motor proteins and methods for	TITLE REFERENCE: 1040. FILE REFERENCE: 1040. CURRENT APPLICATION NUMBER: US/09/724,224 CURRENT FILING DATE: 2000-11-28 PRIOR APPLICATION NUMBER: 09/597,292 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FASTSEQ for Windows Version 4.0	LENGTH: 1115 TYPE: DNA ORGANISM: Human S-09-724-224-1 Query Match 70.7%; Score 1035.4; DB 3; Length 1115;

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GCCCCTGAGAGGCTTCTACCTAGACACAGTCTCGGCACTCAACTTTGCTGCCAGGTCC 1023
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                                                                                                                                                                                                                                                         904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT
                                                                                                                                          844 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCTTGTTGTTTTCGGGACAGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09883096
; Sequence 1, Application US/09883096
; Patent No. 6680369
; GENERAL INFORMATION:
; APPLICANT: Baraud, Christophe
; APPLICANT: Yu, Ming
APPLICANT: Yu, Ming
APPLICANT: Sakowicz, Roman
; APPLICANT: Barel, Umesh A.
; APPLICANT: Davies, Katherine A.
; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
; FILE REFRENCE: 020552-001410US
; CURRENT APPLICATION NUMBER: US/09/883,096
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PATENTIN OF: 2.1
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9.5%; Score 138.6; DB 4; Length '
Best Local Similarity 51.0%; Pred. No. 4.8e-30;
Matches 448; Conservative 0; Mismatches 404; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  1024 AAGGAGGTGATCAATCG 1040
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                                                                                          ; Sequence 1, Application US/10093317; Patent No. 6762043; GENERAL INFORMATION:
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use; FILE REFERENCE: 1040.
; TITLE OF INVENTION: their use; CURRENT APPLICATION NUMBER: US/10/093,317; CURRENT APPLICATION NUMBER: 09/724,224; PRIOR APPLICATION NUMBER: 09/724,224; PRIOR PILING DATE: 2000-11-28; NUMBER OF SEQ ID NOS: 8; NUMBER OF SEQ ID NOS: 8; NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1035.4; DB.4; Length 1115;
Pred. No. 6.9e-292;
0; Mismatches 1; Indels 0;
                1098 AAGGAGGTGATCAATTG 1114
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; ORGANISM: Human
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                                                    fragment
Nucleotide sequence of HsKip3a fragment used
ATPase assay (Figure 5).
                                                                                                                                                                                                                                                                                Length 1152
                 Description of Artificial Sequence: HsKip3a
                                                                                                                                                                                                                                                                        Score 136.6; DB 4; Length
Pred. No. 9.5e-30;
0; Mismatches 389; Indels
                                                                                                                                                                                                                                                                   Query Match 9.3%;
Best Local Similarity 51.2%;
Matches 437; Conservative
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        ; OTHER INFORMATION: D: OTHER INFORMATION: E: OTHER INFORMATION: N: OTHER INFORMATION: N: US-09-883-096-6
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Fatent No. 6880369
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Patel, Umesh A.
TITLE OF INVENTION NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 020552-00141008
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT APPLICATION NUMBER: US/09/883,096
FRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 6
LENGTH: 1152
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Best Local Similarity 50.1%;
Matches 430; Conservative
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ORGANISM: Human
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US-09-724-508-1
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; Sequence 1, Application US/09621233
; Patent No. 6294371
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Breedman, Richard
; TITLE OF INVENTION: No. 6294371e1 motor proteins and metl
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1045
; CURRENT APPLICATION NUMBER: US/09/621,233
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                             Query Match 8.8%; Score 128.8; DB 3;
Best Local Similarity 50.1%; Pred. No. 1.6e-27;
Matches 430; Conservative 0; Mismatches 356;
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LENGTH: 897
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; Patent No. 636881.
; GRENEAL INFORMATION:
; APPLICANT: Breadd, Christophe; APPLICANT: Freedman, Richard; TITLE OF INVENTION: No. 6368841el motor proteins and methods for TITLE OF INVENTION: their use; TITLE OF INVENTION: their use; FILE REPERENCE: 1045; CURRENT APPLICATION NUMBER: US/09/724,508; CURRENT FILING DATE: 2000-11-27; PRIOR APPLICATION NUMBER: 09/621,233; PRIOR PILING DATE: 2000-07-21; NUMBER OF SEQ ID NOS: 2 NUMBER OF SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ 
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Pred. No. 1.6e-27;
0; Mismatches 356;
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Qy 370 CCGCGGCTCTCATGGACCTCCTGCAGAAGGGAGGAGGAGGAGGGCCGAGGCCGGCC	286 GTTCAGACCCTCAACGACCTCTTCCGTGCCATCGAGGAGACCAGCAATGAC	Qy 430 IGGGCCCTITCTGTCACCATGTCTTACCTAGAGATCTACCAGAGAAGGTATTAGACCTC 48:	Db 337 ATGAGATATGAGGTCTCCCTACTACTACTGGAGATCATCAGGATGATCATCGGGACTG 396	397 CTGAACCCTCCGGGCTACCTGGAGCTGCGGGAGGACTCTAAGGGGGTGATCCAGGTG 45	Oy 550 CCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCCTGCCA 605	Db 457 GCCGGCATCACCGAANNNNNNNNNNNNNNNNNNNNNNNNN		Qy 670 GCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTCGCCAGCGAGAGA 725	730		Qy 790 GGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGAAAGTG 845	GTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAGCTC	/UU AI'CAAGGCGACAAGGGIAGCAACAAGTACAACIAICGCGACAGGAAGCTC	0y 904 ACTCGCCTATTGCAGACTCTCTGGGTGGCTCAGCTCAGTATCCTTATTGCCACATT 963	964 GCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 102	Qy 1024 AAGGAGGTGATCAATCGG 1041	Db 880 AAGAACATTAAGACTAGG 897	.565	; Sequence 1, Application US/10090695 ; Patent No. 6664072 ; GENERAL INFORMATION	; APPLICANT: Berauw, Christophe ; APPLICANT: Freedman, Richard ; TILE OF INVENTION: No. 6664072el motor proteins and methods for	; TILE OF TWENTION: CREIT USE ; FILE REPRENCE: 1045 ; CURRENT APPLICATION NUMBER: US/10/090,695	; CURRENT FILING DATE: 2002-03-04 ; PRIOR APPLICATION NUMBER: 09/621,233 ; PRIOR FILING DATE: 2000-07-21 ; NUMBER OF SEO ID NOS: 2	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 1 ; LENGTH: 897	. Humar	; NAME/KEY: misc_feature ; LOCATION: (472)(495)
		577 GCGGCCGCCTGTTCA 592	730 GGAAAACTCTACCTGATTGACTTGGCTGGGGGGGACACGGGGCACAGGCAACAAG 789 593TGATCGACTGGCTGGGTCAGAGGGGGGCGCAAAAAAAAAA		GGGCAGCGTATGAAGGAGGG	850 GTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAGCTC 903		760 ACCCGCTCCTGAAGGACTCTCTGGGAGGAAACAGCCGCACAGTGATGATGATGACTCACTC	AGTCCTGCGAGCAGCAGCCTTCGAGGAGTCCCGGAAACACCTGACCTACGCCGGGCCC	1024 AAGGAGGTGATCAATCGG 1041	880 AAGAACATTAAGACTAAGG 897	SULT 14 -09-724-516-1 Sequence 1, Application US/09724516 Behent No. 6391573	GENERAL NO. 0531103 GENERAL INFORMATION: ADDITIONAL BEALLY CHAILEDED	AFFLICANT: Beraud, Christophe APPLICANT: Freedman, Richard TITLE OF INVENTION: No. 6391573el motor proteins and methods for TITLE OF INVENTION: their use	FILE REFERENCE: 1045 CURRENT APPLICATION NUMBER: US/09/724,516 CURRENT FILING DATE: 2000-11-27	PALOR APPLICATION NUMBER: 09/621,233 PRIOR FILING DATE: 2000-07-21 NIMBER OF SECTIONS: 2	SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID 0.1 LENGTH: 897	TYPE: DNA ORGANISM: Human	: Y: misc feature N: (472)(495) NFORMATION: n = a. C. t. or	יין מ' נ' נ' סד על פין אייני אייני אייני אייני אייני אייני אייני אייני אייני אייני אייני אייני אייני אייני אייני	Best Local Similarity 5.1%; Pred. No. 1.6e-27; Matches 430; Conservative 0; Mismatches 356; Indels 72; Gaps 3;	190 TACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTATGCAGGTTCA 249	30	310 CCCACAGGAGCTGGGAAGACGCACACACAGGCGAGGCCCAGGAGCAACCTGGGGGAACCTGGGGGAATCTGGGGGGAAGCTGGGGGAATCTGGGGGGAAGCCCAGAGCAACCTGGGGGAATCTGGGGGAAGCAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGGAAATGCTGGGGAAATGCTGGGGAAATGCTGGGAAATGCTGGGAAATGCTGGGAAATGCTGGGAAATGCTGGAAATGCTGGAAATGCTGGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTGGAAATGCTAAATGCT	

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964 GCCCCTGAGAGACGCTTCTACCTAGACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 CCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGTGATC 369
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                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                          72;
                                                                                                             Query Match

8.8%; Score 128.8; DB 4; Length 897;
Best Local Similarity 50.1%; Pred. No. 1.6e-27;
Matches 430; Conservative 0; Mismatches 356; Indels 72
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; OTHER INFORMATION: n = a, c, t, or US-10-090-695-1
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Patent: US 6387644-A 7 14-MAY-2002;
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Unpublished

Staline, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Direct Submission

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Pusion(TW) cloning system between the Sall and Hindil sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'Hindil site to maintain reading frame.

Clone distribution: http://bioinfo.clontech.com/orfclones.
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Cloning of human full-length CDSs in BD Creator(TM) System Donor
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/lab host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
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/db_xref="taxon:9606"
/clone="GH00245X1.0"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"Conding N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., and Farmer,A.

"Phelan,M. and Farmer,A.

"Direct Submission

"Labmitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow

"Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the

Harvard Institute of Proteomics. Each CDS has been cloned in two

forms: with and without stop-codon (to allow fusion with C-terminal

tag). The CDS has been directionally cloned using BD In-Fusion(TM)

cloning system between the Sall and HindIII sites of the pDNR-DUAL

vector. Additional sequences in the clone: 'ACC' after Sall site

and before 'ATG' to provide Kozak consensus sequence; 'GG' after

last codon and before HindIII site to maintain reading frame.

Location/Qualifiers
                                                                                                                                                   1998 bp mRNA linear SYN 13-MAY-2003
Synthetic construct Homo sapiens kinesin-like 4 mRNA, partial cds.
BT007888
FLI CDNB
                                                                                                                                                                                                                          FLI_CDNA.
synthetic construct
synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 1998)
Kalnine,N., Chen,K., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinga,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                   /clone_1ch="GH0024511.0"
/clone_1ib="BD Creator(TM) CDS Library derived from MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collection"
/lab_host="DHSalpha T1 resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
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EPBEKAEDCWELQISPELLAHGRQXILDLINEGSARDLRSLQR HGPFSQVEDLERVEGITGKQMESFLKANILGLAAGGRCGASL" MATCh 99.6%: Score 1458: DR 12. Length 19	Best Local Matches 145	QY 4 GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCCACCTCCAGCTCGCGTAAGG 63 DD 76 GGTCGCTGTCGGCTAAGCAAGATTGCAACTCGTCGTCCACCTCCAGCTCGCGTAAGG 135	Oy 64 GTGGCTGTGCGACTGCGGCCATTTGTGGAACAGCGGGAGCAAGTGATCCCCCCTGT 123	Oy 124 GTGCGGGGCATGGACACTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT 183 Db 196 GTGCGGGGCATGGACAGCTGCTCTAAGAGTTGCTAACTGGAGGAACCACCAGGAGAACT 255	Qy 184 CTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGTACTCAGCAGGACATCTATGCA 243 Db 256 CTCAAATACCAGTTTGATGCCTTCTATGGGAGAGAGAGTACTCAGCAGGACATCTATGCA 315	Qy 244 GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC 303 1	OY 304 TATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG 363 Db 376 TATGGACCCACAGGAGCTGGGAAGACGCACACACACAGGCAGCCCAGAGCAACCTGGG 435	Oy 364 GTGATCCCGGGGCTCTCATGGACCTCCTGCAGGTCAGAGGAGGAGGGGGGGC 423 Db 436 GTGATCCCGCGGGCTCTCATGGACTCCTGCAGCTCACAAGGAGGAGGAGGAGGAGGGGCCGAGGCC 495	OY 424 CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA 483	Oy 484 GACCTCCTGGACCTGCTTGGTAATCCGAGACTGCCGGGGGAATATC 543 Db 556 GACCTCCTGGACCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC 615	0y 544 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC 603 0	OY 604 CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGC 663 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 664 AGTCATGCTGTGCTCCTGGTCAAGGTGGACGGAAAGTTTGGCCCCATTTCGCCAG 723	Oy 724 CGAGAGGAAAACTCTACCTGATTGACTTGGGTGAGGGTCAGGGACAACGGGGGCACAGGC 783 Db 796 CGAGAGGGAAAACTCTACCTGATTGACTTGGGTCAGAGGACAACCGGCGCACAGGC 855	Oy 784 AACAAGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGC 843	Qy 844 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGACAGCAGCAGCTC 903 Db 916 AAAGTGGTAGATGCGCTGAATCAGGCCTCCCTCGTGTACCTTATCGGGACAGCACC 975	QY 904 ACTEGECTATTGCAGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963 Db

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Homo sapiens mRNA for kinesin-like DNA binding protein, complete
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Tokai-Nishizumi,N. and Edamasu,M.

Direct Submission

Bubmitted (10.5EP-1998) Noriko Tokai-Nishizumi, The University of Submitted (10.5EP-1998) Noriko Tokyo.

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(E-mail:tokai/appc.ims.u-tokyo.ac.jp, Tel:03-5449-5302,

D38751:Submitted (10.7Nov-1994)

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Kid; kinesin-like DNA binding protein; kinesin family.
HOMO sapiens (human)
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/clone="pBSkid"
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25. .2022
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Massiello,C., Maskeri,B., Mastrian,S.L., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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/ db_xref="id="LocusID:3835"

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Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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6. .2003
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/gene="KIF22"
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GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG
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                                                                   GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCTGT
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LLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLBRLLSLDRLL
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HGPFSQVEDLERVEGITGKQMESFLKANILGLAAGQRCGAS"
                     DNA Sequencing by Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Transonen Saeedi, UR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: f Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817. Location/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone lib="NIH MGC_7"
/lab_host="DH10B-R"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:1573 IMAGE:3535435"
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/gene="KIF22"
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1. (bases 1 to 2134)

2. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

3. Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

3. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

4. Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scaplecton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Wanny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Bouterfield, Y.S., Krzywinski, M.I., Shalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
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1324 CGAGAGCGGATGCTGATGAGACAGTAGAAGAGAGAGAGCTTTTTTTT	BC003427 Mus musculus kinesin family member 22, mRNA (cl INARS:2615715), complete cds. BC003427. GI:13097359 Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Musmalia; Butheria; Rodentia; Sciurognathi; Musmalia; Butheria; Rodentia; Sciurognathi; Musmalia; Butheria; Rodentia; Sciurognathi; Musmalia; Butheria; Rodentia; Sciurognathi; Musmalia; Bransberg, R.L., Feingold, E.A., Grouse, L.H., D Klausner, R.D., Collins, F.S., Magner, I., Shenmes, Alltechia, R.F., Jordan, H., Moore, T., Mark, I. Tos Scapetz, T.E., Brownstein, M., J. Usdin, T.B., Tos Scapetz, T.E., Brownstein, M., Ju Gain, T.B., Tos Scapetz, T.E., Mullahy, S.J., Bosak, S.A., McCley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Iu, Fahey, J., Helton, E., Garcia, A.M., Gay, L.J., Iu, Fahey, J., Helton, E., Ketteman M., Madan, A., Rous, Sanchez, A., Milting, M., Madan, A., Young, A.C., Sancher, A., Schein, J.B., Schestiev, M. Toudman, A., Rob Sanchez, A., Milting, M., Madan, A., Young, A.C., Schenting, S., Schergren, E.J., Ju, Fahey, J., Helton, E., Ketteman M., Young, A.C., Schenting, S., Schergren, E.J., Ju, Fahey, J., Helton, E., Ketteman M., Young, A.C., Schenting, S., Schergren, E.J., Ju, Fahey, J., Helton, E., Ketteman M., Young, A.C., Schenting, E., Schercren, S.J. and Marra Generation and initial analysis of more than 1 luman and mouse cDNA sequences Jetting, S., Karywinski, M.I., Skalska, U., Schenin, J.B., Schercren, S.J. and Marra Ornect Under Collection (MGC), Cancer Genomics Office, Institute, 31 Center Drive, Room 11A03, Bethes USA MIH-MGC Project URL, http://www.hgc.bcm.tmc.edu/cdna/Contact: MGC help desk Edwarding Center codes EOM-HGS Contact: MGC help desk Edward, Inh. R.J., Muzhy, A., Mushi, R.J., Muzhy, A., Mushi, R.J., Muzhy, R.J., Martin, R.G., Muzhy, A.N., Gibbs, R.A. Contact: amg@bcm.tmc.edu Gonescial A.M., Lu, X., Hulyk, Kowis, C.R., Sneed, A.J., Martin, R.C., Muzh, K., Mark, M., Gibbs, R.A.	
6	RESULT 9 BC003427 LOCUS LOCUS LOCUS ACCESSION VERYWOLDS SOURCE ORGANISM AUTHORS TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE TITLE COURNAL REFERENCE TITLE COURNAL REMARK COMMENT	
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n. Derge, J.G.,
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alaefer, C.F., Bhat, M.K.,
..., Mang, J., Hsieh, F.,
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Toshiyuki, S.,
anc, N.A., Peters, G.J.,
cRwan, P.J.,
Richards, S.,
..., Hulyk, S.W.,
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M., formation can be found nttp://image.llnl.gov AAGGCTGAGGAAAAGGAG 1443 |||||||||||||||| NAGGCTGAGGAAAAGGAG 1534 inear ROD 29-JUN-2004 (cDNA clone MGC:6456 ς, S.W., Loulseged, H., γ, D.M., Nanavati, TAGAGATTGAGAGGCTT 1383 bbrata; Euteleostomi; Auridae; Murinae; Mus. of Health, Mammalian e, National Cancer esda, MD 20892-2590, , Inc. Bortium (LLNL) ine Human Genome -16903 (2002)

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ILIANIAPERRFYQDTISALNFTARSKEVINRPFTNESLQPHALAPVKLGQKELLGPS
                 sequencing because it: matched mRNA gi: 21704181.
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Series: IRAK Plate: 5 Row: m Column: 7
This clone was selected for full length s
passed the following selection criteria:
                                                                                                                                   'db_xref="taxon:10090"
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Patent: US 6387644-A 1 14-MAY-2002;
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Pred. No. 1.6e-266;
0; Mismatches 1; Indels 0;
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Patent: US 638764-A S 14-MAY-2002;
Location/Qualifiers
1. .1041
/organism="unknown"
/mol_type="unassigned DNA"
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McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Milvova, T., Menga, V., Murkphy, T., Naylor, J., Nguyen, C., Northu, C., Norman, C.H., O'Comnor, T., O'Donnell, P., O'Nasil, D., O'Comnor, T., O'Comnor, T., Rejoc, R., Nguyen, C., Redock, R., Respec, R., Rejoc, R., Rejoc, R., Rejoc, R., Regoc, R., Rogock, R., Schauer, S., Schuback, R., Schauer, S., Schuback, R., Schauer, S., Schuback, R., Stanger Homanin, V., Stojanovic, N., Strauss, N., Subramain, A., Talames, J., Teefaye, S., Theodore, J., Viel, R., Wold, R., Wilson, B., Wux, Naman, D., Yew, W.J., Young, G., Jainon, J., Zembek, L., Zimmer, A. and Zody, M. Trigilio, J., Vassiliev, H., Viel, R., Wilson, B., Wux, Wawman, D., Yew, W.J., Young, G., Jainon, J., Zembek, L., Zimmer, A. and Zody, M. Oiter, Submister, G., Lander, B., Masham, C., Lander, B., Masham, C., Lander, B., Masham, C., Lander, E., Abuelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barria, N., Bastien, V., Bloom, T., Boughalavity, L., Boukhgalter, B., Cork, R., Cook, R., Cook, P., Corum, B., Dakrellann, K., Baro, S., Graham, L., Grand-Pietrer, N., Haffez, N., Hagopian, D., Hagos, B., Hall, Y., Horton, L., Hulme, W., Ilfez, N., Matchen, R., Maylor, J., Morch, L., Hulme, W., Ilfez, N., Matchen, R., Maylor, J., Horton, L., Hulme, W., Ilfez, N., Watchen, R., Marches, C., McCarthy, M., Medonald, P., Mereus, L., Manning, J., Matthews, C., McCarthy, M., Medonald, P., Meneus, L., Match, R., Matchen, R., Marches, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Match, R., Mat
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Web site: http://www-seq.wi.mit.edu
Contect: sequence submissions@genome.wi.mit.edu
Contect: sequence submissions@genome.wi.mit.edu
Center project Information
Center clone name: 158 A 6
Center clone name: 158 A 6
Center clone name: 158 A 6
Center clone name: 158 A 6
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150558 bases at least Q40
Consensus quality: 150654 bases at least Q20
Insert size: 151000; agarcse-fp
Insert size: 150041; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
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Mus musculus clone RP24-158A6, WORKING DRAFT SEQUENCE, 4 unordered
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boquslawkiy, L., Boukhgalter, B., Chorn, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., Dakrellano, K., Dewar, K., Dlaz, J.S., Dodges, S., Farco, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                             GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
                                                                                                                                                               GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
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AC101919.4 GT:28951338
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mus musculus
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Mus musculus chromosome 1, clone RP24-344C18, complete sequence.
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Biran, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bogualavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
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Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 1, clone RP24-344C18
Unpublished

2 (bases 1 to 164759)
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  TGTGCTCCTGGTCAAGGTGGACCAGCGGAACGTTTGGCCCCCATTTCGCCAGCGAGGG
                                                                                  AAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACC----GGCGCACAGGCAACA
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17 84394: contig of 41558 bp in length
18 84494: gap of 100 bp
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Location/Qualifiers
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Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Cook, A., Cook, P., Corum B., DeArellano, K., Cook, A., Cook, P., Corum B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Mahova, T., Mlenga, V., Murphy, T., Naylor, J., Nouyen, C., Nicol, Y., Peterson, K., Phunkhang, P., Pierre, N., O'Neull, D., Oliver, J., Peterson, K., Phunkhang, P., Fise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stolanovic, N., Stubbs, M., Vassilliev, H., Voha, Lander, J., Topham, K., Travers, M., Vassilliev, H., Voha, C., Viel, R., Voha, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, M., Viel, 
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                           Perreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gords, S., Goyette, M., Graham, L., Gard-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illiev, I., Johnson, R., Jones, C., Kamat, A., Katlas, A., Kells, C., Larocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, J., Marthews, C., McCarthy, M., McEwan, P., McReran, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G., Direct, Submission
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DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
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Pred. No. 1.8e-224;
0; Mismatches 282;
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complement(34455.35895)
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Best Local Similarity 78.4%;
Matches 1116; Conservative
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1119 ATAATTGTGCCTGTTTGTGGATGAAGAGAGAAGGAAGGAGGAGCACCCCTGTGTACGAGC 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 GCGACTGCGGCCATTTGTGGATGGAACAGCGGGGCAAGTGATCCCCCCTGTGTGCGGGG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1179 TIGIATAAGCAAGGIAGGGATIGGCTGTCGTCTTCTAGCTGGAGTAAGGGTGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     821 TCAGACTCTCCCAGACCTCCTGCACCTAACAAGGGAAGAGAATGCTGAGGGCTGGCCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           999 TCAGTTTGATGCCTTCCATGGAGAGAGACACTCAGTGGGGACATCTATGTAGGTTTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 CACAGGAGCTGGGAAGACGCACACAATGCTGGGGCAGCCCAGAGCAACCTGGGGTGATCCC
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consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                      /clone="RP24-275J1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%; Score 740.6; DB 2; 78.2%; Pred. No. 1.1e-186; ive 0; Mismatches 249;

    .297639
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Best Local Similarity 78.2
Matches 916; Conservative
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167809
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                                                                                                                                                                                                       S Litzen, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastian, V., Bogulavkiy, L., Boukhgaler, B., Choepel, A., Canagel, M., Colling, S., Collymore, A., Cooke, P., Canagel, M., Collins, S., Collymore, A., Cooke, P., Cooke, P., Patzalano, K., Dewar, K., Diaz, J. S., Dodge, S., Earo, S., Cooke, P., Dakallano, K., Dewar, K., Diaz, J. S., Dodge, S., Earo, S., Gooke, P., Dakallano, K., Dewar, K., Diaz, J. S., Dodge, S., Earo, S., Gooke, P., Dakallano, K., Dewar, K., Diaz, J. S., Dodge, S., Gooke, P., Dakallano, K., Dewar, K., Diaz, J. S., Dodge, S., Gookete, M., Carlane, L., Grand-Pierre, M., Gooke, C., Kanat, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A., Katatas, A
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Center: Whitehead Institute/MIT Center for Genome Research
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                                                                                                                        Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 1, clone RP24-275J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seg.wi.mit.edu
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Center clone name: 275_J_1
       musculus (house mouse)
                                                                                                    (bases 1 to 297639)
                                                                                                                                                                                               (bases 1 to 297639)
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                                                                                                                                                                   Unpublished
  SOURCE
ORGANISM
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AUTHORS
TITLE
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, N., Allen, N., Anderson, S., Arachchi, H.M., Banra, N., Bastien, V., Anderson, S., Arachchi, H.M., Banra, N., Bastien, V., Anderson, S., Arachchi, H.M., Banra, N., Bastien, V., Bloom, T., Edungalavi, J., Bouhdgalter, B., Cormus, B., Chang, J., Collymore, A., Cook, A., Cooke, S., Dooley, K., Dorris, L., Dearellano, R., Diaz, J.S., Dodge, S., Dooley, K., Dorris, J., Barcken, J., Radon, P., Farce, S., Perreira, P., Fitzgerald, M., Gage, D., Galagan, J., Grander, M., Kartes, A., Kells, C., Landers, T., Lowinson, R., Jones, C., Ramat, A., Kartes, A., Kells, C., Landers, T., Lowinson, R., Jones, C., Ramat, A., Kartes, A., Kells, C., Landers, T., Lowinson, R., Jones, C., Ramat, A., Kartes, A., Kells, C., Landers, T., Lowinson, R., Jones, C., Ramat, A., Kartes, A., Kells, C., Landers, T., McCarthy, M., Meldrim, J., Menus, J., Mihova, T., Mienga, V., McCarthy, M., Meldrim, J., Menus, J., Melman, J., Schupback, R., Sewery, P., Romen, J., Schupback, R., Sewery, P., Romen, J., Schupback, R., Sewery, P., Smith, C., Spencer, B., Stange-Thomann, V., Schupback, R., Stanger, S., Sander, S., Schupback, R., Stanger, S., Mannin, J., Schupback, J., Stonger, S., Stanger, rbu,C., Norman,C.H., O'Connor,T., O'Donnall,P., O'Neil,D.,
Ollver,J., Petergon,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Scaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassillev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Slinnoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (33-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/MIT Center for Genome Research Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 196674)
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Mus musculus chromosome 1, clone RP23-202A19, complete sequence.
ACI02127
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Birran, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 1, clone RP23-202A19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AGGTGATTAACCAGGCTTTCACCAAAGCGAGTGTACAACCTCAGGCCTTGACACCTGTTA
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                                                                                                                     641 AGGCCTCACACAGAAGCCCATCACTAGTTTCTCTGACTTCGAGAAGCACTTCCTAGT
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48.3%; Score 706.8; DB 10; Length 196674;
Best Local Similarity 73.3%; Pred. No. 1.2e-177;
Matches 1013; Conservative 0; Mismatches 357; Indels 12; G Complement (10373. 11559)
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665 GTCATGCTGTGTCCTGGTCAAGGTGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGC 724
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Search completed: November 10, 2004, 13:18:11 Job time: 6475.64 secs

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

9, 2004, 09:45:10 ; Search time 756.977 Seconds (without alignments) 10152.424 Million cell updates/sec November Run on:

US-10-797-893-7 Title: Perfect score:

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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4134886 segs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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geneseqn2002as: *
geneseqn2002bs: * geneseqn2003as:* N_Geneseq_23Sep04:* geneseqn2001as:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

	Description		Adc23343 DNA encod	Adq60233 Human mic		Add60229 Human mic	Add09241 Human KNS	Adk40995 Novel hum	Aaf15853 Human pro	Adc23341 DNA encod	Add60231 Human mic	Adc23337 DNA encod	Adq60227 Human mic	Abk70260 Human lun	Aas38879 Novel hum	Ach44493 Human foe	Ach77408 Human gen	Ach91108 Human gen	Adm01564 Human CDN	Ado44181 DNA encod	Adj95073 Novel NOV	Abx34596 Human mdd	Aba94614 Human kin
SUMMARIES	ID		ADC23343	ADQ60233	ADC23339	ADQ60229	ADQ09241	ADK40995	AAF15853	ADC23341	ADQ60231	ADC23337	ADQ60227	ABK70260	AAS38879	ACH44493	ACH77408	ACH91108	ADM01564	ADO44181	ADJ95073	ABX34596	ABA94614
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æ	Query Match		100.0	100.0	99.8	99.8	99.6	98.8	98.6	70.9	70.9	70.7	70.7	32.8	25.7	18.1	15.9	15.7	12.7	12.7	10.7	10.6	9.5
	Score		1464	1464	1461	1461	1458	1447	1443.2	1038.4	1038.4	1035.4	1035.4	480	376.4	265	233.2	230.4	185.6	185.6	156.8	154.8	138.6
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Abs57215 Human kin Adj95077 Novel NOV Aba94616 Nucleotid Abs57216 DNA encod	Aai70088 Human kin Aai39619 DNA encod Adm81051 Human HeK Abv47991 Human pro Abv47991 Human pro	Abq73061 Human kin Aal56806 DNA encod Adb66788 DNA encod Abq73062 Human kin	Ad156807 DNA encod Adb66787 DNA encod Add28568 Human kin Add10109 Human NOV Abg01615 Human NoV	Add19012 Human sof Abl28591 Drosophil Abl16733 Drosophil Abl16732 Drosophil Add30338 Human nov Add30569 Human nov
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ALIGNMENTS

RESULT 1

DNA encoding the human kinesin-like DNA binding protein (KID) (SegID 7). ADC23343 standard; DNA; 1464 BP. (first entry) 18-DEC-2003 ADC23343; ADC23343

human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodilator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.

Homo sapiens

/*tag= a /product= "KID protein" Location/Qualifiers 1. .1464 /*tag= a

US6387644-B1.

14-MAY-2002.

28-NOV-2000; 2000US-00724224.

20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292.

(CYTO-) CYTOKINETICS INC.

Beraud C;

WPI; 2003-706919/67. P-PSDB; ADC23344.

Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.

Disclosure; SEQ ID NO 7; 26pp; English

900 900 960

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1321 AAGCGAGAGGGGATGGTGCTAATGAAGACAGTAGAAGAAGAAGAACCTAGAGATTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321 AAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAAGAAGGACCTAGAGATTGAGAGG
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                                                                                                                     CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC
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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular compounds for the treatment of cellular compounds for the treatment of cellular compounds for mediate agents that are are capable of modulating the activity of target proteins having motor companies, such that the target protein directly or indirectly produces ADP composphate. Furthermore, this activity can be determined using composphate. Furthermore, this activity can be determined using compositive modulators of the target protein, which is a method that identifies modulators of the target protein, which is a communomodulators and antiinflammatories. Accordingly, through gene compositive therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polymuclectide sequence is human KID DNA (SeqID 7) encoding a full length companies.
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100.0%; Score 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candiate agents that bind to a target protein, modulators of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune conflication induced after medical procedures including surgery and proliferation induced after medical procedures including a human microtubule motor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                               New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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                                                                                                                                   20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
                                                                                          06-MAR-2002; 2002US-00093317
                                                                                                                                                                                                                                   (CYTO-) CYTOKINETICS INC.
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P-PSDB; ADQ60234.
US6762043-B1
                                              13-JUL-2004
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                                                                    Gaps
                                  Query Match
100.0%; Score 1464; DB 12; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0;
Sequence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                    /transl except= (pos: 4. .5; aa: Pro)
/note= "This codon has an apparent 1 nucleotide deletion
that alters the reading frame"
                                                                                                                                                                         encoding the human kinesin-like DNA binding protein (KID) (SeqID 3)
                                                                                                                                                                                                 human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate agent as modulator of function of a targ protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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99.8%; Score 1461; DB 10; Length 1538;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 0; Indels 0;
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/*tag= a
/product= "KID protein"
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Location/Qualifiers
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20-JUN-2000; 2000US-00597292.
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P-PSDB; ADC23340.
                                                                                                ADC23339 standard;
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                  GETCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCACGCTCGCGTAAGG
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                                                  GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGACGAAGCAAAAAAGAACTGGAGGCCAAGATGTTGGCCCAGAAGGCTGAGAAAAGGAG
                          GTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACAGAGGCAAAGAAGAGCCCGAGGCCCT
                                                                                  GAGGAAGAAGAGTTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTGCCTCCCAGAAA
                                                                                                             GAGGAAGAGAGAGTTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTGCCTCCCAGAAA
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activity, a method of testing for APPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restencesis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restencesis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft resisting, MID and for treating autoimmune diseases, arthritis, graft resisting, inflammatory bowel disease and angioplasty. This sequence represents DNA encoding a human microtubule motor protein of the invention. Note: The specification states that this encourage the protein featured as SEQ ID NO:4, but this does not
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encoding cDNA SEQ ID NO:426. ADQ09241 standard; cDNA; 2097 (first entry) 23-SEP-2004 Human KNSL4 ADQ09241;

THAP responsive element; angiogeneeis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator; thanatos-associated protein; THAP; THAP responsive gene; THAP family;

WO2004055050-A2 Homo sapiens

The present invention describes a method for modulating the expression of a thantos (dasth)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a mucleic acid, and so enhancing or repression the expression of the THAP responsive gene. Also described. (1) a method competing a manacription of a gene responsive to a THAP responsive competing a than responsive competing a transcription of a THAP responsive element. (4) a cell comprising a transcription factor decoy described and a consisting a transcription factor decoy described and a THAP-family polypeptide or its biological fragment. (3) a transcription factor of decoy described and a THAP-family polypeptide or its biological fragment. (5) methods of modulating the interaction between a nuclet acid and a THAP-family polypeptide or its biological fragment; (6) a weetor packaging cell line comprising a transcription factor decoy described by a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-family polypeptide (6) a method of ameliorating complex; (6) a vector packaging cell which expresses a recombinant into the nucleus; (10) methods for reduction mediated by a THAP/chemokine complex; (7) methods of identifying a test compound that modulates transcription cassociated with a condition mediated by a THAP/chemokine or an insufficient appropriate, cardiovascular for reduction the compression or activation cassociated with a condition metastasis of a cnecrous tissue, excessive or insufficient appropriate appropriate pronocter operably linked to a nucleic acid comprising a THAP responsive pronocter operably linked to a nucleic acid comprising a promocra described above or that expresses and neurodegeneration comprising a thyperpride or its biological fragment; (13) an involvement or insufficient conding a metastable product operably linke appression or activation conding a detectable product (12) a responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic a cancerous tissue, excessive insufficient apoptosis, cardiovascular disease or neurodegenerative seases. The present sequence is used in the exemplification of the expression of a Thanatos (death)-Associated Protein (THAP) Clouaire T; diseases. The present sequence is used in the inflammation, metastasis of Example 47; SEQ ID NO 426; 612pp; English. ΣÌ Roussigne (ENDO-) ENDOCUBE SAS. (CNRS) CNRS CENT NAT RECH SCI 10-DEC-2002; 2002US-0432699P. 03-JUL-2003; 2003US-0485027P. 10-DEC-2003; 2003WO-IB006434 J, Amalric F, WPI; 2004-525034/50. P-PSDB; ADQ09240 01-JUL-2004 Modulating responsive Girard

Sequence 2097 BP; 483 A; 592 C; 628 G; 394 T; 0 U; 0 Other;

Gaps ö DB 12; Length 2097; Indels ; 0 99.6%; Score 1458; D 100.0%; Pred. ... 0; Mismatches Query Match Best Local Similarity 100. Matches 1458; Conservative

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QY 1084 GTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAAGACCCGAGGCCCT 1143 Db 1180 GTTAAGCTGTCTCAGAAAGATTGCTTGGTCCACCAGAGGACAAAGAGAGCCCGAGGCCCT 1239 QY 1144 GAGAAGAGAGATTGCATGGTCCACCAGGACACAAGAGACCCCCAGAAA 1203 Db 1240 GAGAAGAGAGATTGGAGCCTGAGCCCTGGCTCCAGCTCTGCCTCCCCAGAAA 1299 QY 1204 CTCAGCCCCTACAGAGCCTAGGCCCATGGCAGCCTCTGCCTCCCCAGAAA 1299 QY 1204 CTCAGCCCCTACAGAGCTAAGCACATGGAGCCCTTGCTCTCTCCTCAGC 1359 Db 1300 CTCAGCCCCTACAGAGCTAAGCAGCACCAGGCCATGCTGAGCCTCTCTCT	RESULT 6 ADK40995 ID ADK40995 ID ADK40995 standard; DNA; 2099 BP. XX AC ADK40995; XX XX DT 06-MAY-2004 (first entry) XX DT 06-MAY-2004 (first entry) XX DT of-MAY-2004 (first entry) XX Cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; XX Cytostatic; immunomodulator; cardiant; fungicide; ophthalmological; XX Cytostatic; protipheral nervous system; XX Cytostatic; protipheral nervous system; XX CANCET; peripheral nervous system; XX Alzheimer's disease; Parkinson's disease; multiple solerosis; XX Alzheimer's disease; Parkinson's disease; multiple solerosis; XX Alzheimer's disease; majoriancy pain; sexual dysfunction; mood disorder; XX Alzheimer's disorder; cognition disorder; dyskinesia; XX XX XX XX XX XX XX XX XX XX XX XX XX	(SUDA/) SUDARSANAM SUTARIANAM STIGOTIEV IV, SUDARSANAM STIGOTIEV IV, SUDARSANAM SUDARSANAM STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV STIGOTIEV
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a naturally cocurring kinase polypeptide; (b) is a encodes a naturally occurring kinase polypeptide; (d) encodes the copypeptide in (a), except that it lacks one or more, but not all, of an N-terminal domain, c-terminal catalytic domain, a catalytic domain, a colled-coil structure region, a spacer region and a C-terminal domain, a colled-coil structure region, a spacer region and a C-terminal domain, a colled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, collypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or euronal-associated diseases, and metabolic disorders. The disorders are parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, coviral infections, infections caused by prions, ocular diseases, migraines, pain, excual dysfunction, mood disorders, attention disorders, cognition disorders, dyskinesias, metabolic disorders and organ transplant rejection. This sequence corresponds to the DNA encoding one of the invention.

Sequence 2099 BP; 484 A; 592 C; 628 G; 395 T; 0 U; 0 Other;

GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG Gaps ï Query Match 98.8%; Score 1447; DB 10; Length 2099; Best Local Similarity 99.9%; Pred. No. 0; Matches 1458; Conservative 0; Mismatches A. 7-3-3

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760 363 460 423 520 483 580 543 640 603 700 663 280 243 340 303 400 101 GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG 160 123 220 GTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT 183 CTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTATGCA CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAAGGTATTA crearrecessrerecessassecearcastaserrecestraterrates CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGC CTCAAATACCAGTTTGATGCCTTCTATGGGGAGGAGGAGTACTCAGCAGGACATCTATGCA gerrcagrecadecearceradecacrificades de da antecea de de contra de c TATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCCAGCCCAGAGCAACCTGGG GTGATCCCGCGGGGCTCTCATGGACCTCCTGCAGGCTACAAGGGAGGAGGGTGCCGAGGGC GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC CTGATICCGGGICTCTCCCAGAAGCCCATCAGIAGCIIIGCTGAITITIGAGCGGCACTIC GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCCTGT 701 341 461 484 544 641 604 64 191 221 184 244 304 401 364 424 521 581 124 281

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                                                                                                                                                 encoding the human kinesin-like DNA binding protein (KID) (SeqID 5)
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Pred. No. 3.1e-278;
0; Mismatches 1; Ir
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                                                                 ADC23341 standard; DNA; 1041 BP
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Best Local Similarity 99.9%;
Matches 1039; Conservative (
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2000US-00597292
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                                                                                                                        (first entry)
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ADQ60231 standard; DNA; 1041
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New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                            Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                     "Human microtubule motor protein #3"
                           Human microtubule motor protein DNA #3.
                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 5; 26pp; English
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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The invention fraction to invention mistoring with the invention fraction to invention fraction to invention also relates to a method of screening acids encoding them. The invention which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, modulators of the target protein, modulators of the target cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders as in infilammation, for treating disorders associated with kinesin-like DNA confideration disorders such as cancer, hyperplasias, restenosis, cardiac proliferation disorders such as cancer, hyperplasias, restenosis, cardiac proliferation disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders and inflammation, for treating disorders consecuted with KID and for inhibiting KID and for treating disorders and diseases, arthritis, graff rejection, inflammatory bowel disease and consecution induced after medical procedures including angery and consecution induced after medical procedures including a human microtubule invention relates to human microtubule motor proteins and the nucleic

Sequence 1041 BP; 228 A; 295 C; 302 G; 216 T; 0 U; 0 Other;

Length 1041;

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                                                            1 ATGGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCGTCCACCTCCAGCTCGCGTA
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                              1; Indels
Score 1038.4; DB 12;
Pred. No. 3.1e-278;
0; Mismatches 1; II
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               Best Local Similarity
Matches 1039; Conserv
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61 AGGGTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGGCGAAGTGATCCCCCC 120

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1020 1020 240 120 180 300 300 360 420 420 480 480 540 540 9 900 999 99 720 720 780 780 840 840 900 900 960 960 TGTGTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAG **ACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTAT** ACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTAT GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGTTT GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTT GCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAT GCCTATGGACCCACAGGAGCTGGGAAGACGCACAATGCTGGGCAGCCCAGAGCAACCT GGCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTA Gecegecardescerricateaceargretraceragagareraceagagara TTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAGACTGCCGGGGGGAAT Tracaccrecrecaccerectrecegagaccrecrarrecgagagacrecegeggaar TTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCC Troctidocadocadrogadarogadorogadocadocadocadocadocadocadocado CGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGC cecaercarecrerecresreaageresaccaeceseaacerresecearringe CAGCGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACA CAGCGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACA GGCAACAAGAGGCCTTCGGCTAAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCCCCCTGTTTGTCT GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG GGCAAAGTGGTAGAAGTGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGG ATTGCCCCTGAGAGACGCTTCTACCTAGACACACACTCCGCACTCAACTTTGCTGCCAGG TCCAAGGAGGTGATCAATCG 1040 rccaaggaggrgarcaarrg 1040 ATCCTGATTCCGGG1 61 181 841 196 1021 121 121 181 241 241 301 301 361 361 421 421 481 481 541 601 721 721 781 781 841 901 961 1021 601 661 661 901 ò 셤 ઠે ద ઠ ద ò g ð g ઠે g ò ద ò 셤 셤 ò 8 g ò g 8 a ઠે g 8 셤 ò 셤 à

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                                            DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 1)
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Pred. No. 2.2e-277;
0; Mismatches 1; Ir
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/product= "KID protein"
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Best Local Similarity 99.9%;
Matches 1036; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase activity, a methods of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such accorder, hyperplasias, restenoisis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders and inflammation, for treating disorders proliferation disorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune disorders and inflammation, modulatory bowel disease and proliferation induced after medical procedures including surgery and anglophasty. This sequence represents DNA encoding a human microtubile modulation of the invention of the invention when the content of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                           Human; microtubule motor protein; gene; ds; cellular prollferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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99.9%;
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Matches 1036; Conserv
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                                                                                                                                                                                                       Homo sapiens
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The invention relates to new polymucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS35943-AAS39333 represent novel human diagnostic and therapeutic coding
                                                                                                                                                                                                                                                    1356 AGAGAAGGACCTAGAGATTGAGAGGCTTAAGACGAAGCAAAAAGAACTGGAGGCCAAGAT 1415
                                                                                                        1236 CCCGGCCATGCTGGAGCGCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGAGCCA 1295
                                                                                                                             300 CCCGGCCATGCTGGAGCGCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGAAGCCA 359
                                                                                                                                                                                                     360 GGGGCCCCTCTGTTGAGTACCCCAAAGCGAGAGGGGGATGGTCTAATGAAGACAGTAGF 419
                                                                                                                                                                                                                                                                         180 ACCAGAGGCAAAGAGAGCCCGAGGCCCTGAGGAAGAGGAGATTGGGAGCCCTGAGCCCAT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic;
                                                                                                                                                                               1296 GGGGGCCCCTCTGTTGAGTACCCCAAAGCGAGAGCGGATGGTGGTGCTAATGAAGACAGTAGA
                                                        240 GGCAGCTCCAGCCTCTGCCTGCCTGAAACTCAGGCCCCCTACAGAAGCTAAGCAGCATGGA
                                       GGCAGCTCCAGCCTCCCAGAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garcia PD, Sudduth-Klinger J;
Pot D, Kassam A, Lamson G;
I, Drmanac S, Labat I;
nes WL, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; 118 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic and therapeutic gene #1937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.7%; Score 376.4; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Escobedo J, Innis MA, Garcia | Radazzo F, Kennedy GC, Pot D, Crkvenjakov R, Dickson M, Drmanu D, Kita D, Garcia V, Jones WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 1080; 1193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS38879 standard; cDNA; 386 BP.
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                                                                                                                                                                                                                                                                                                                               1416 GTTGGCCCAGAA 1427
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                                                                                                                                                                                                                                                                                                                                                                 480 GTTGGCCCAGAA 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-530177/58.
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Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS38879;
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                                          1176
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide comprising a sequence selected from 183 human DNA sequences (appearing as ABK70130-ABK70312), or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the colypeptides. Also included are an expression control sequence; a host cell transformed or transfected with an expression control sequence; a host cell transformed or transfected with an expression vector of; an isolated contibiod, or its antipod, or its antipod, or tits antipod, or tits antipod for detecting the presence of a cancer in a patient; a fusion protein comprising at least the polypeptide; an oderately colypeptide; a method for setimulating and/or expanding T cells stringent conditions; a method for setimulating and/or expanding T cells specific for a tumour protein; an isolated T cell population comprising T component consisting of carriers and immunostimulate, and a second component selected from the polynucleotides, proteins, and a second component selected from the polynucleotides, proteins, antibodies, fusion proteins. T cell populations and antigen presenting cells expressing the component in a patient by administering the composition and diagnostic kits comprising at least one of the oligonucleotide of, or an antibody and cetection reagent consisting of a reporter group. The polypeptides are useful as vaccines for the treatment or prevention of polynucleotides are useful as vaccines for the treatment or prevention of the polynucleotides may be used as probes or primers for nucleic acid compunitation and integer presenting cells can be used to etimulate or expand T cells specific for a tumorous protein. The present sequence is one of the 183 lung cancer associated comply and in the present sequence is one of the 183 lung cancer associated compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1055
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                                                                                                                                                                                                                                                                                                                    New tumor lung proteins and nucleic acids encoding the proteins, useful as vaccines and for treating, preventing, diagnosing or monitoring lung
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Pred. No. 5.3e-123;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 144; 189pp; English
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10-OCT-2000; 2000US-0239440P.
29-JUN-2001; 2001US-0301928P.
                                                                                                    20-SEP-2001; 2001WO-US042232
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                                                                                                                                                                                                                                                  Benson DR, Mohamath R,
                                                                                                                                                                                                                                                                                    WPI; 2002-372001/40:
                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                     WO200224057-A2
                                                                     28-MAR-2002.
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                                                                                                                                                                   240
                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide comprising any one of
                                                      9
                                  CCTTGGGACCTGTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAG
                                              CCCGAGGCCCTGAGGAAGAGGAATTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTG
                                                                                      61 CCCGAGGCCCTGAGGAGAGAGAGATGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTG
                                                                                                          CCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAGC
                                                                                                                                                                181 GCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGGAGCCAGGGGGCCCCCTCTGTTGA
                                                                                                                                                                                   GTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAAGAAGGACCTAGAGA
                                                                                                                                                                                                    GTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAAGAAGAACCTAGAGA
                                                                                                                                                                                                                       TTGAGAGGCTTAAGACGAAGCAAAAAAAGAACTGGAGGCCAAGATGTTGGCCCAGAAGGCTG
                                                                                                                                                                                                                                          TTGAGAGGCTTAAGACGAAGCAAAAGAACTGGAGGCCAAGATGTTGGCCCAGAAGGCTG
                                                                                                                           121 CCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAAGCAGCATGGACCCGGCCATGCTGGAGC
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Human; 88; sequencing by hybridisation; SBH; expressed sequence genome mapping; biodiversity; genetic disorder.
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                                                                                                                                                GCCTCCTCAGCTTGGACCGTCTGCCTTGCCTCCCAGGGAGCCAGGGGGGCCCCT
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                 Indels
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Pred. No. 3.2e-94;
                                                                                                                                                                                                                                                           AGGAAAAGGAGAACCATTGTCCCACA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 31705; 44pp; English.
                                                                                                                                                                                                                                                                       AGGAAAAGGAGAACCATTGTCCCACA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stache-Crain B,
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                                                                                                                                                                                                                                                                                                                                                                                 Human foetal brain cDNA #5218.
                                                                                                                                                                                                                                                                                                                           ACH44493 standard; cDNA; 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2001; 2001US-00918995.
       98.48;
                                                                                                                                                                                                                                                                                                                                                               13-OCT-2003 (first entry)
                 380; Conservative
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STACHE-CRAIN B.
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense DNA or RNA
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      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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(LABA/)
(STAC/)
(DICK/)
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determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/RST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPPO at sequence. The sequence contained in electronic format directly from USPPO at sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 464;
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18.1%; Score 265; DB 9; Length 46
Best Local Similarity 77.6%; Pred. No. 3.5e-63;
Matches 333; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 464 BP; 96 A; 136 C; 131 G; 96 T; 0 U; 5 Other;
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16-OCT-2003.

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Penn SG, Rank DR, Hanzel DK;
    03-APR-2002; 2002US-00029386.
          03-APR-2002; 2002US-00029386
                                WPI; 2004-119264/12.
               (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                             surveying tissues.
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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for

Claim 15; SEQ ID NO 10603; 80pp; English.

The invention relates to a mucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide superences in the specification, or their complements or fragments, and sequences in the specification. The probe is a single exon probe that this defined in the specification. The probe is a single exon probe that the probes sunder high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-defined in human cells or tissues. Also included are a spatially-defined in human cells or tissues. Also included are a spatially-comprising a plurality of single exon nucleic acid molecule and addressable set of single exon nucleic acid probes for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon nicroarray for measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid of any of the above-mentioned amino acid of sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, contiguous and oracids of any of the above-mentioned amino acid of a customer desiring to measure gene expression, a method of provading a customer desiring to measure gene expression data by subscription, and a computer-readable storage medulum which contains a database having a plurality of records cated above. The probes methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying a customer detect the presence of expression of a shigle exon microarrays.

Conted above, the probes are used in identifying and characterising gross alterations in the probes are used in identifying and contains a detecting and characterising gross alterations in the genomic locus that included second in identifying the sequence is a human single exon probe of the invented peptide. The sequence desired in a prince and peptide co patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704

684 CAAGGIGGACCAGCGGGAACGIITGGCCCCAIIITGGCCAGGGGAAAAACICIACCI Gaps 0; DB 12; Length 531; 3; Indels Query Match 15.9%; Score 233.2; DB 17 Best Local Similarity 98.7%; Pred. No. 2.6e-54; Matches 235; Conservative 0; Mismatches 3

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Sequence 531 BP; 117 A; 153 C; 149 G; 112 T; 0 U; 0 Other;

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93

34 ccaddriggaccadcdgaaacgrrrggccccarrrcgccadcdagagaaaacrcraccr 744 GATTGACTTGGCTGGGTCAGAGACAACCGGCGCACAGGCAACAAGGCCCTTCGGCTAAA 94 GATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAAGAGAAGAAGAGCCTTCGGCTAAA 153 AGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA

154 AGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA 213 음 à g

Search completed: November 10, 2004, 06:58:00 Job time: 760.977 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein 5, 2004, 18:34:12; Search time 75.9417 Seconds (without alignments) 1747.786 Million cell updates/sec November Run on:

US-10-797-893-2 1878 Title: Perfect score:

1 MAAGGSTQQRRREMAAASAA......FYLDTVSALNFAARSKEVIN 370 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 Total number of hits satisfying chosen parameters:

2002273 segs, 358729299 residues

Searched:

length: 0 length: 2000000000 seq Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* Database :

geneseqp1980s: geneseqp2000s: geneseqp2001s: geneseqp2001s: geneseqp2002s: geneseqp2003bs: geneseqp2003bs: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de				
Result		Query				
No.	Score	Match	Length	8	ID	Description
1	1878	100.0	370	7	ADC23338	Adc23338 Human kin
7	1878	100.0	370	80	ADQ60228	Adq60228 Human mic
m	1878	100.0	490	7	ADK40973	Novel
4	1878	100.0	665	œ	ADQ09240	_
S	1873	99.7	512	7	ADC23340	Нишап
9	1873	99.7	512	80	ADQ60230	Adq60230 Human mic
7	1763	93.9	346	7	ADC23342	Adc23342 Human kin
80	1763	93.9	346	Φ	ADQ60232	Adq60232 Human mic
σ	1763	93.9	460	m	AAB56650	0
10	1763	93.9	487	7	ADC23344	
11	1763	93.9	487	æ	ADQ60234	Human
12	559.5	29.8	784	4	ABB71112	Abb71112 Drosophil
13	559	29.8	548	7	ADM04007	Adm04007 Human pro
14	559	29.8	966	œ	AD044167	Ado44167 Structura
15	552.5	29.4	357	S	AAU76958	Aau76958 Novel hum
16	552.5	29.4	868	4	ABU53123	Abu53123 Intracell
17	552.5	29.4	868	S	AAU76957	Aau76957 Novel hum
18	552.5	29.4	868	7	ADC31082	Adc31082 Human nov
19	552.5	29.4	868	7	ADI15915	Adil5915 Human PP
20	551.5	29.4	603	9	ABU11606	Abull606 Human MDD
21	549	29.5	908	ស	AAU76967	
22	541	28.8	408	æ	ADN40550	Adn40550 Candida a
23	541	28.8	408	œ	ADN40554	Adn40554 Candida a
24	541	28.8	972	ω	ADN40548	Adn40548 Candida a
25	541	28.8	974	ω	ADN4 0552	Adn40552 Candida a

Abb65183 Drosophil	Human	Abb07410 Human kin	Abg72052 Human kin	Human	Human	Aau79592 Human HsK	Human	_	Human	Human	Adb80468 Ovarian c	_	Human	Adq20128 Human sof	Human	-	Human	Adj95078 Novel NOV
ABB65183	ABG72053	ABB07410	ABG72052	AAE14401	AAE14402	AAU79592	ADC31540	AAE14400	AAU79590	ABR48222	ADB80468	ADC35116	ADL83290	ADQ20128	ADQ09226	AAU19569	ABP51294	ADJ95078
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535.5	528 528	528	528	526	526	226	526	526	526	526	526	526	526	526	526	525.5	525.5	523.5
26	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytoëtatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. Human kinesin-like DNA binding protein (KID) (SeqID 2). /note= "Encoded by ATGCA" Location/Qualifiers ADC23338 standard; protein; 370 AA. 28-NOV-2000; 2000US-00724224. 20-APR-1999; 99US-00295612 20-JUN-2000; 2000US-00597292. (first entry) (CYTO-) CYTOKINETICS INC. WPI; 2003-706919/67. N-PSDB; ADC23337. Key Misc-difference Homo sapiens; US6387644-B1. 18-DEC-2003 14-MAY-2002. ADC23338; Beraud C; ADC23338

Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.

Claim 1; SEQ ID NO 2; 26pp; English.

This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS 300
domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 2) of the invention.
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                                                                                                                                                                                   Length 370;
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100.0%; Pred. No. 3.8e-182;
ive 0; Mismatches 0;
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                     Best Local Similarity 100.
Matches 370; Conservative
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                                                                                                                                                          Sequence 370 AA;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein, and methods of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor protein useful for treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                               New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1878; DB 8;
100.0%; Pred. No. 3.8e-182;
iive 0; Mismatches 0;
                                                                                                                                                                                  Claim 1; SEQ ID NO 2; 26pp; English.
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Matches 370; Conservative
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                                                      WPI; 2004-532491/51
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ADK40973;

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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and encodes a naturally occurring kinase polypeptide; (d) encodes the coopypeptide in (a), except that it lacks one or more, but not all, of an N-terminal domain, a creatlytic domain, a C-terminal catalytic domain, a C-terminal catalytic domain, a C-terminal catalytic domain, a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, colypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the creatural or peripheral nervous system, Alzheimer's diseases, con parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by fungi, ocular diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, neurological disorders, netrological disorders, neurological disorders, netrological disorders, neurological disorders diseases, neurological disorders,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . This sequence corresponds to one of the kinase polypeptides of
                                                                                                                                                          cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotenelve; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and
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100.0%; Pred. No. 5.9e-182;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 80; 491pp; English.
                                                                                                        Novel human kinase protein #80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-2001; 2001US-0343169P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUDA/) SUDARSANAM S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-587115/55.
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                                                                                                                                                                                                                                                                              Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for modulating the expression of a thanatoe (death) -associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
                         SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGGN
                                                                                                                                                                                                                    QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS
                                                                                   ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIY
                                                                                                                             QEKVLDLLDPASGDLVIREDCRGNILIPGLSOKPISSFADFERHFLPASRNRTVGATRLN
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SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQN
                                                              ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thanatos-associated protein; THAP; THAP responsive gene; THAP family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 47; SEQ ID NO 425; 612pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ09240 standard; protein; 665 AA
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Best Local Similarity 100. Matches 370; Conservative

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Length 490;

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1 MAAGGSTOORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA 9 MAAGGSTQQRRKEMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA

the expression of the THAP responsive gene. Also described: (1) a method cf modulating the expression of a gene responsive to a THAP chemokine complex; (2) a pharmaceutical carrier; (3) a transcription factor decoy element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a cell comprising a transcription factor decoy described above; (5) methods of comprising a transcription factor decoy described above; (5) methods of polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a viral vector which comprises a promoter operably linked co a nucleic acid encoding a THAP-family polypeptide or its biological ercombinant THAP-family polypeptide; (8) a method of constructing, a cell which expresses a respectated with a condition mediated by a THAP/chemokine complex; (5) methods of identifying a test compound that modulates transport of a THAP responsive element or that modulates the transport of a sasociated with a condition selected from excessive or insufficient associated with a condition selected from excessive or insufficient appropriae, cardiovascular disease and neurodegenerative conspicution associated with a condition resulting the symptoms associated with transcriptional repressive or insufficient cappotosis, cardiovascular disease and neurodegenerative contints associated with transcriptional repressive or insufficient comprising a theorem or THAP-family polypeptide in an individual; (11) a vector expension of a THAP responsive promoter operably linked to a mucleic acid comprising a detectable product; (12) a genetically engineered call comprising the vector described above or that expression or activation reaction comprising and an RAP polymerses, and in invited to a mucleic comprising the vector described acid comprising a number of described acid comprising a number of described acid angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the reducing symptoms of conditions such as excessive or insufficient present invention

Seguence 665 AA;

ö ORSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS 300 QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS 300 LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360 SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHILEGQN 120 121 ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLBIY 180 QEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLN 240 1 MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA 60 1 MAAGGSTOORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA Gaps ö Length 665; 0; Indels 100.0%; Score 1878; DB 8; 100.0%; Pred. No. 9.5e-182; ive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 370; Conservative FAARSKEVIN 370 61 181 181 241 241 301 301 361 61 셤 g ò g ð g ò g Ś ò

human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate. Human kinesin-like DNA binding protein (KID) (SeqID 4). /note= "Encoded by CA" Location/Qualifiers ADC23340 standard; protein; 512 AA. 20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. 28-NOV-2000; 2000US-00724224. (first entry) (CYTO-) CYTOKINETICS INC. 361 FAARSKEVIN 370 WPI; 2003-706919/67. N-PSDB; ADC23339 Misc-difference Homo sapiens US6387644-B1 18-DEC-2003 14-MAY-2002. Beraud C; ADC23340; RESULT 5 ADC23340 g

This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor or phosphate. Furthermore, this activity or be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatorise. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperasias, trestenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 4) of the invention.

Claim 1; SEQ ID NO 4; 26pp; English.

Sequence 512 AA;

ö 61 2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS ö DB 7; Length 512; Indels ö 99.7%; Score 1873; DB 7; larity 100.0%; Pred. No. 2e-181; Conservative 0; Mismatches 0 Similarity Best Local Sim Matches 369; Query Match

DPPCVRGMDSCSLBIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGGNA 121 62

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein, and act as a target protein, modulators of the target protein, and methods of treating candiar proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA
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                                              SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 182
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                                                                                                                                    RSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL 302
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DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 122
                                                                                                                     RSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL 301
                                                                                                                                                                                                                                                                                                                                                                                               Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                        SVLAYGPTGAGKTHTWLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ
                                                                                   EKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQ
                                                                                                                                                                                 FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNP
                                                                                                                                                                   FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF
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                                                                                                                                                                                                                                                                                                                                                                         Human microtubule motor protein #2.
                                                                                                                                                                                                                                                                                                   ADQ60230 standard; protein; 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                  AARSKEVIN 370
                                                                                                                                                                                                                                WPI; 2004-532491/51
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binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:3, but this does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Score 1873; DB 8; Length 5 100.0%; Pred. No. 2e-181; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human kinesin-like DNA binding protein (KID) (SegID 6).
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20-JUN-2000; 2000US-00597292.
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Best Local Similarity 100.
Matches 369; Conservative
                                                                                                                                                                                                                                                                                                                    appear to be the case.
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 512 AA;
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Homo sapiens
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                                                                                                                                                                                      pystems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 6) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, microtubule motor protein, cellular proliferation disorder; cancer; hyperplasia, restenosis, cardiac hypertrophy, immune disorder; inflammation, kinesin-like DNA binding protein, KID; autoimmune disease; arthritis, graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                     Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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                                                                                                                                                                                This invention relates to a novel method for high throughput
                                                                                                                                                                                                                                                                                                                                                                                         93.9%; Score 1763; DB 7; Length 346; 100.0%; Pred. No. 1.8e-170;
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                                                                                                                                                        Claim 1; SEQ ID NO 6; 26pp; English
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Best Local Similarity 100.
Matches 345; Conservative
(CYTO-) CYTOKINETICS INC
                                                   WPI; 2003-706919/67.
                                                                                                                                                                                                                                                                                                                                                                   Sequence 346 AA;
                                                              N-PSDB; ADC23341
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                         Beraud C;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding procein (KID) and for inhibiting KID. The sequences are used for creating for modulators of motor proteins useful for treating disorders and inflammation for treating cancer, hypertrophy, immune disorders and inflammation, for treating disorders or proliferation disorders and inflammation, for treating disorders and inflammation, for treating disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders and inflammatory bowel disease and proliferation induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and consideration induced after medical procedures including surgery and consideration induced after medical procedures including surgery and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consideration and consid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
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93.9%; Score 1763; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.8e-170;
Matches 345; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 6; 26pp; English.
                                                                                                                                                                                                                                                                                                        2000US-00597292.
                                                                                                                                                                                                                                                                  99US-00295612.
                                                                                                                                                                         06-MAR-2002; 2002US-00093317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYTO-) CYTOKINETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004-532491/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-532491/
N-PSDB; ADQ60231.
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                                                                                                                                                                                                                                                                  20-APR-1999;
                                                                                                                                                                                                                                                                                                                 20-JUN-2000;
28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation.
US6762043-B1
                                                                                    13-JUL-2004
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neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins, called prostate cancer antigens, given in AAB5535 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, valnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polymucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57031 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        issociated gene sequences, referred to as prostate cancer for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                                                                      cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                Human prostate cancer antigen protein sequence SEQ ID NO:1228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 460;
                   TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 93.9%; Score 1763; DB 3;
Best Local Similarity 99.4%; Pred. No. 2.8e-170;
Matches 345; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 1649-1651; 2338pp; English.
                                                                                                                               AAB56650 standard; protein; 460 AA
                                                                                                                                                                                                                                                                                      prostate cancer; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000; 2000WO-US005988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer associated antigens, useful for treatmench as prostate cancer.
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-587513/55.
N-PSDB; AAF15853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200055174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1999;
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326
                                 302
                                                                                                                                                                     AAB56650;
                                                                                                           AAB56650
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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 8) of the invention.
                                                                                                           263
                                                                                                                                                                                 323
                                                                                                                                             241
                                                                                                                                                                                                      ETLKYQFDAFYGEXSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodilator; antiinflammatory; gene therapy; cytostatic; cardian; restenosis; cellular prollferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                   PGVI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG
                                                          NILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF
                                                                                                           NILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF
                                                                                                                                                                                 ROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a candidate agent as modulator of function of a targ protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                            302 KLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNPAARSKEVIN 348
                                                                                                                                                                                                                                                      KLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human kinesin-like DNA binding protein (KID) (SeqID 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 8; 26pp; English
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                                                                                                                                                                                                                                                                                                                                                                                 ADC23344 standard; protein; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-2000; 2000US-00724224.
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20-JUN-2000; 2000US-00597292,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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N-PSDB; ADC23343.
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24 GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQ

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BTLKYQPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ

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acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target cancer, hyperplasias, restenois, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular corrections, immune disorders and inflammation, for treating alsorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune cassociated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                        26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                                                                                                                         2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGWDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEI YQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                  Length 487;
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                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 40128
                                                                                                                                                                                                                                                                                                               Match 93.9%; Score 1763; DB 8; I Local Similarity 100.0%; Pred. No. 3.1e-170; les 345; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB71112 standard; protein; 784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                         Sequence 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
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                                                                                                                                                            145
                                                                                                                                                                                                                     205
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                                                                                                                                                                                                                                             122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                                                                                                                                                                                                                                       REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 325
                                                                                                                                                                             Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restencis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                    85
                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                                                                                                            LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                             LI PGLSQKPI SSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                  26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                    2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQET
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Pred. No. 3.1e-170;
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                                 93.9%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human microtubule motor protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ60234 standard; protein; 487 AA
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2000US-00597292.
2000US-00724224.
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                                                                           Conservative
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                                                        al Similarity
345; Conserv
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                  Sequence 487 AA;
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20-JUN-2000;
28-NOV-2000;
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                                           Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                           61 KEORKVFTYDAAYDASATOTTLYHEVVFPLVSSVLEGFNGCIFAYGOTGTGKTFTMEGVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDCRGN-ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQ 256
                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABR2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                        ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RERLAPPROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 TRRP------PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN
                                                                                                                                                                                                                                                                                                                                                                              5 SRRPGTGSSQTPNECVQVVVRCRPMSNRERSERSPEVVNVYPNRGV----VELQNVVDGN
                                                                                                                                                                                                                                                                                                                                    31; Gaps
                                                                                                                                                            invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                    Disclosure; SEQ ID NO 40128; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                              Length 784;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                           Query Match 29.8%; Score 559.5; DB 4; Best Local Similarity 39.8%; Pred. No. 2.9e-47; Matches 141; Conservative 56; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein of the invention SEQ ID NO:2692.
                                   Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM04007 standard; protein; 548
                                  Li PWD,
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                                 Adams M,
           CORP NY
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                                                                  N-PSDB; ABL15215
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           (PEKE ) PE
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24-SEP-2003.

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Ishii S;
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PDFTATQEMVYQATTKSLIEGVISGYNATVFAYGPTGCGKTYTMLGTDQEPGIYVQTLND 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel human polynuclectide and the encoded polypeptide. A polynuclectide of the invention may have a use in gene therapy. An oligonuclectide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynuclectides as a probe for detecting the polynuclectide. The polynuclectides ADM01316-ADM01376 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating thair expression and activity, or as a target of gene therapy. The proteins ADM01759-ADM06201 encoded by the polynuclectides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                    Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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12-APR-2002; 2002EP-00008400
                                                                                               22-MAR-2002; 2002JP-00137785.
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Matches 132, Conservative
                                                                                                                                                                                                                                                                                               Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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AC ADO.
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cell proliferative disorder; cancer; atherosclerosis; viral infection; HIV; neurological disorder; Parkinson's disease; Alzheimer's disease;
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95. .325
note = kinesin motor domain
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469
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489
/note= "potential phosphorylation site"
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97. .399
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148. .287
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                                                                                                                                                             63. .647
/note = kinesin motor domain
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/note = .
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The present sequence represents a structural and cytoskeleton-associated polypeptide (SCAP). The SCAP polypeptides and polynucleotides of the invention are useful for diagnosing, preventing or treating diseases or conditions associated with aberrant expression of SCAP, such as cell
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Chien D, Lu DAM, Yang YG, Yue H, Murage J, Griffin JA, Burrill JD;
Wang JT, Marquis JP, Blake JJ, Chawla NK, Lee S, Becha SD, Lee SY;
Richardson TW, Bhatia UG, Zheng W, Sprague WW, Tang YT, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human structural and cytoskeleton-associated proteins and polynucleotides for diagnosing, preventing or treating diseases associated with aberrant protein expression, e.g. cancer,
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                                                             note= "leucine zipper pattern"
                                    "leucine zipper pattern"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2002; 2002US-0414227P.
18-NOV-2002; 2002US-0427594P.
07-FEB-2003; 2003US-0445724P.
07-MAR-2003; 2003US-0453277P.
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N-PSDB; ADO44181.
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              infections (e.g. HIV) or neurological disorders (e.g. Parkinson's disease, Alzheimer's disease or stroke). These may also be used for assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are also useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329
                                                                                                                                                                                                                                                                                                                                                                  271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 STINAKEIMQLLMKGNRQRTQEPTAANQTSSRSHAVLQVTVRQRSRVKNLLQEVRQGRLF 247
                                                                                                                                                                                                                                                                                                                                              94 YGERSTQQDIYAGSVQPILRHILLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD 153
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/label= SwitchI motif
/note= "Responsible for sensing of the gamma phosphate
and initiating the conformational change between ATP and
ADP bound forms of the enzyme"
                                                                                                                                                                                                                                                                           RVRVAVRLRPF--VDGTAGAS-----DPPCVRGMDSCSLEIANWRNHQETLK-YQFDAF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarthritic; antiinflammatory; varoceart, mincutobupgressive; cardiac hypertrophy; cellular proliferation disease; hyperplasis; restenosis; cancer; solid tumour; carcinoma; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; surgery; angioplasty; nanotechnology; GeneChip array; expression monitoring; human; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ--REGKLY
                                                                                                                                                                                                                                             16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP to
   cancer or atherosclerosis), viral
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                                                                                                                                                                                                       Query Match 29.8%; Score 559; DB 8; Length 998; Best Local Similarity 38.9%; Pred. No. 4.8e-47; Matches 132; Conservative 70; Mismatches 121; Indels
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part of the nucleotide-binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 QDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 368
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/label= ATP/GTP_binding_site_motif
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 proliferative disorders (e.g.
                                                                                                                                        activity of the polypeptide.
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(1). (1) is useful for screening addulators of Hakipad. The method concentration, and assaying for the level of Hakipad activity, where the concentration, and assaying for the level of Hakipad activity, where the Hakipad activity is from binding activity or Arpase activity, where the change in activity between the test and control concentration indicates a modulator. A composition containing (1) is useful in the treatment of inflammation, cardiac hypertrophy, cellular proliferation diseases e.g. hyperplasias, restenosis, cancer, including solid tumours of skin, brain, lung, heart, bone, genitourinary tract, liver, nervous system, adrenal glands, haematologic, gynaecological and testicular carcinomas, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease, proliferation induced after medical procedures, such as surgery, angioplasty. The motor domains may also be used in nanotechnological applications, and polymucleotides encoding the proteins is further useful for inclusion on GeneChip (RTM) array or for use in expression monitoring. This is the amino acid sequence of the novel human contor protein Hakipad motor domain, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                 Novel microtubule motor protein for screening modulators of HsKip3d, useful in treatment of hyperproliferative disease e.g. cancer, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease.
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/note= "Responsible for sensing of the gamma phosphate
and initiating the conformational change between ATP and
ADP bound forms of the enzyme"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGV1PRALMDLLQLTREEGAEGRPWALSVTMSYLE1YQEKVLDLLDPASGDLV1REDCRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 MKVVVRVRPENTKEKAAGFHKVVHVVDKHILVFDPKQEEVSFFHGKKTTNQNVIKKQN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated novel human microtubule motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.4%; Score 552.5; DB 5; 39.7%; Pred. No. 4.5e-47; ive 59; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Fig 3; 66pp; English.
                                                                                                                                                                               03-AUG-2001; 2001WO-US024285.
                                                                                                                                                                                                                      03-AUG-2000; 2000US-00632344.
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                                                                                                                                                                                                                                                           (CYTO-) CYTOKINETICS INC.
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les 141; Conservative
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N-PSDB; ABK10348.
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244 SINONVRIAKMSLIDLAGSERASTSGAKGTRFVEGTNINRSLLALGNVINALADSKRKNO 303

314 GLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 368

PFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL-----NQ

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304 ---HPYRNSKLTRLLKDSLGGNCQTIMIAAVSPSSVFYDDTYNTLKYANRAKDI 355

Search completed: November 5, 2004, 18:44:37 Job time : 78.9417 secs

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query

No. Score Match Length DB ID

2 2467 95.3 487 16 US-10-797-893-4

2 2467 95.3 487 16 US-10-797-893-8

4 2151 83.1 460 9 US-90-255-300-1228 Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1528, Appli Sequence 1532, Appli Sequence 1532, Appli Sequence 1532, Appli Sequence 1532, Appli Sequence 1532, Appli Sequence 1532, Appli Sequence 1532, Appli Sequence 1532, Appli Sequence 33219, 112 578.5 22.3 1237 15 US-10-425-115-332919 Sequence 33219, 112 578.5 22.3 1237 15 US-10-425-114-370 Sequence 33, Appli 13 574.5 22.2 1232 14 US-10-116-712-670 Sequence 670, Appli

Seguence 2153, Ap		Sequence 62748, A	Sequence 231231,	26	82	32	2, Ap	16,		142,	16	664,	699	314,		316,	2, App	Sequence 1, Appli	H.	Ä	306	25,		ý	23,	112,	17	ý	7	47	Sequence 474, App
5 US-10-408-765A-2153	US-10-334	US-10-4	US-10-425	US-10-1	US-10-146-473-82	US-1	S US-10-332-089-2	US-10	US-1	5 US-10-287-226-142	US-1	US-10-116-712-664	US-1	US-1	US-1	S US-10-363-829-316		US-09-847-874A-1		US-1	S US-10-287-226-306	US-1	US-1	US-1	US-10-	us-	US-10-	US-10-	US-10-601-		US-10-282-174-474
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22.2	22.2	22.0	21.9	21.8	21.7	21.7	21.7	21.7	21.6	21.6	21.5	21.5	21.5	21.5	21.3	21.3	21.2	21.1	21.1	21.1	21.1	21.0	21.0		21.0	٠.	20.9	20.7	20.6	20.5	20.5
574.5	574.5	569	266	564.5	561	561	561	561	260	559.5	557.5	557.5	557.5	557	552.5	552.5	550	546.5	546.5	546.5	545.5	544.5	•	543	543	4	•	535	٠	532	532
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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61 ASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQ 120
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; Sequence 4, Application US/10797893
; Sequence 4, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud. Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; FILE REFERENT APPLICATION WIMBER: US/10/797,893
; CURRENT APPLICATION NUMBER: US/09/724,224
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR PILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; WUMBER OF SEQ ID NOS: 8
; SEQ ID NOS: 8
; SEQ ID NOS: 8
; SEQ ID NOS: 9
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Best Local Similarity
Matches 512; Conserv
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US-10-797-893-4
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    242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
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Publication No. US20040009549A1

GENERAL INFORMATION:

APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH

APPLICANT: SUDARSANAM, SUCHA

TITLE OF INVENTION: METHADD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: METHADD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: WINASER IDENTIFIED WITH THE METHOD

FILE REFERENCE: 038602/1543

CURRENT APPLICATION NUMBER: 0/10/334,143

CURRENT APPLICATION NUMBER: 60/2-12-31

FRIOR APPLICATION NUMBER: 60/343,169

FRIOR FILING DATE: 2001-12-31

NUMBER OF SEQ ID NOS: 207

SOFTWARE: PATENTIN VET. 2.1

SOFTWARE: PATENTIN VET. 2.1
                                               TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                                                                   VKLSQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
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                                                                        362 VKLSQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
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100.0%; Pred. No. 6.6e-195;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 479; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            NHCPTM 512
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                                                                                                    181 YOEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRL
ASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKD
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95.3%; Score 2467; DB 16; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.9e-199;
Matches 486; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10797893
; Dublication No. US20040142397A1
; GENERAL INFORMATION:
    APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; FILE REFERENCE: 1004
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 LEIERLKTKOKELEAKMLAQKAEEKENHCPTM 512
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US-10-797-893-8
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                   423 ASOKLSPLOKLSSMDPAMLERLLSLDRLLASOGSOGAPLLSTPKRERMVLMKTVEEKDL
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                                                                                                                                                              APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAlo1
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 1228
LENGTH: 460
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Pred. No. 2.3e-172;
1; Mismatches 17; Indels
                                                                                                    Sequence 1228, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
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95.9%;
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Matches 424; Conservative
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63 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 122
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Sequence 6, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud.
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/597,224
; FRIOR FILING DATE: 2000-11-28
; FRIOR FILING DATE: 2000-06-20
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100.0%; Pred. No. 4.6e-149;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 369; Conservative
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Sequence 15901. Application US/10437963

Sequence 15901. Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Burbaruk, Brad

APPLICANT: Burbaruk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 159031
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                                                                                                                                         LDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSH
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US-10-437-963-159031
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LOCATION: (1)..(377)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Oryza sativa
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con Young J.
APPLICANT: The Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of t
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                                                                                                                                                                                                                                                                                                                                                     68.1%; Score 1763; DB 16; Length 346; 100.0%; Pred. No. 7.8e-140; ive 0; Mismatches 0; Indels 0
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US-10-425-115-320209
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 345; Conservative
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US-10-797-893-6
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LENGTH: 589
                                                                                                                                     LENGTH: 346
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Los Vocalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 332919
LENGTH: 783
                                                  403 ARGPEEERIGSPEPMAAPASASOKLSPLOKLSSMDPAMLERLLSLDRLLASOGSOGAPLL 462
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                             KGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIA
                                                                                                                                348 PERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPVKLSQKELL----GPPEAKR
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OTHER INFORMATION: unsure at all Xaa locations
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; Publication No. US20040214272A1
; GENERAL INFORMATION:
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LOCATION: (1)..(
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 103943
LENGTH: 776
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                                                                                                                                                           QLKGLAWVPVRSLEEFHEIYSIGVQRRKVAHTGLNDVSSRSHAVLSIRITT-----DV 220
                                                                                                                                                                                                                           ECYKLDAFFGQESRVCEIFDQEVSAVIPGIFEGTNATVFAYGATGSGKTYTMQGTEDLPG 117
                                        147 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 206
                                                                                                                     207 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 266
                                                                                                                                                                                                   267 REGKLYLI---DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRD 323
                                                                                                                                                                                                                                                                                   SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA 383
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                                                                                                                                                                                                                                                                                                                                                                 384 LGPVKLSOKELLGPPEAK-----RARGPEE----EEIGSPEPMAAPASASQ 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INPORMATION: Clone ID: PAT_MRT4530_101324C.1.pep
US-10-437-963-103943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 103943, Application US/10437963
; Publication No. US200401233431
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brabazuk, Brad
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; ORGANISM: Homo sapiens
US-10-334-143-33
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US-10-116-712-670
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING PATE: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NOS: 73128
LENGTH: 854
FAARSKEV---INRPFTNESL--OPHALGPVKLS-OKE--LLGPPEAKRARGPEEEIGS 413
                     414 PEPMAAPASASQKLISPLQKLISSMDPAMLERLLISLDRILLASQGSQGAPILLS----TPKRER 469
                                                                                | : | | : | | : | 581 AEAQLLASKTBPQRSPAPSHVSTPGSTQRKTRRSILAAGGGNYFSKLDSKRHAADNAQV 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 GTVFCYGATGAGKTYTMLGTMENPGVMVLAINDLFSKVTQKNH-----SIKLSYLEIY 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%; Score 578.5; DB 15; Length 854; 32.9%; Pred. No. 2e-39; Live 94; Mismatches 205; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: LIB3689-256-H1_FLI.pep
US-10-425-114-59708
                                                                                                                         470 MVLMKTVEEKDLEIERLKTKQKELEAK 496
                                                                                                                                                    641 RELORKVSTLESEIEKMK-KEHLLOLK 666
                                                                                                                                                                                                                                Sequence 59708, Application US/10425114
Publication No. US20040034888A1
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Gao, Yongwei
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Best Local Similarity
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ORGANISM: Zea mays
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: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 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                                                                                                                                                                         324 SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFINESLQPHA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 SKLTRILQDSIGGNSHTIMIACVSPADSNILEETLSTLRYADRARKIKNKPIVN--IDPHT 351
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Sequence 33, Application US/10334143

Sequence 33, Application US/10334143

Publication No. US20040009549A1

GENERAL INPORMATION:
APPLICANT: GRICORIEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REWOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543
CURRENT APPLICATION NUMBER: US/10/334,143

CURRENT APPLICATION NUMBER: 60/343,169

PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207

SOFTWARE: PALENTIN VEY: 2.1

SEQ ID NO 33

LENGTH: 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VRVALKCRPLVPKEISEGCQMCLSFVPGETQVVVGTDK------SFTYDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIREDCRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 İKİVGLTEKTVLVALDITVSCLEQGNNSRİVASİAMNSQSSRSHAIFTISIEQRKKSDKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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LLSLDRLLASOGSOGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKOK-ELEAKMLAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 1237;
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                                                                                                             | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
470 MVLMKTVEEKDLEIERLKTKQKELEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 670, Application US/10116712; Publication No. US20030194764A1
```

Fri Nov 12 12:26:23 2004

OM protein - protein search, using sw model

5, 2004, 18:34:12 / Search time 10.0875 Seconds November Run on:

(without alignments)
3300.235 Million cell updates/sec

Perfect score: Sequence:

US-10-797-893-6 1768 1 MGRCRLSKIGATRRPPPARV.....FYLDTVSALNFAARSKEVIN 346

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

* Query Score Match Length	% Query Match Le	F.	ngth	DB	SUMMAKIES	Description
87.7 665 2	87.7 665 2	8	2 S6	S6	S62328	kinesin-like DNA b
33.6 664 2	33.6 664 2	~	7 T	È	T48258	kinesin-like prote
31.4 784 1	31.4 784 1	-		×	A55236	kinesin-related pr
31.1 703 2	703 2	0		4	A86319	F25116.11 protein
30.9 1254 2	1254 2	7		-	T18277	kinesin heavy chai
30.3 784 2	784 2	7		-	T40594	probable kinesin-l
30.1 1226 2	30.1 1226 2	7		-	151617	kinesin-like prote
30.0 885 2	30.0 885 2	7		ш	D86151	F22M8.8 protein -
29.8 1388 2	29.8 1388 2	7		Н	T30335	KLP2 protein - Afr
1070 2	29.7 1070 2	~		۲	T06733	kinesin homolog F2
29.6 1056 2	29.6 1056 2	7		Ξ	H84777	probable kinesin-r
29.6 1058 2	29.6 1058 2	7		-	T47525	kinesin-related pr
1006 2	29.5 1006 2	7		۲	T02017	kinesin-related pr
29.2 1076 2	29.2 1076 2	7	2 E	ш	B84687	
29.1 699 1	699 1	-	7	S	S38982	kinesin-related pr
4 29.1 1066 1	1066 1	-	-	F	A48669	kinesin-related pr
29.1 1695 2	29.1 1695 2	N	7	~	A56921	kinesin family pro
513.5 29.0 701 1 B	29.0 701 1	н	-	-	B44259	kinesin-related pr
29.0 805 2	29.0 805 2	~	~	٠,	S64238	ש
29.0 1225 2	29.0 1225 2	7	7	~	A56514	
747 1	29.0 747 1	-		~	A57107	kinesin-related pr
28.9 1022 2	28.9 1022 2	7		щ	E84792	
28.8 786 2	28.8 786 2	7		4	A53939	kinesin homolog KH
28.8 2954 2	2954 2	0		۲	T14156	kinesin-related pr
28.7 1229 2	1229 2	~		Н	T48959	kinesin-like prote
28.7 1231 2	1231 2	N	•	ď	A54803	microtubule-associ
28.7 928 2	928 2	~	-	H	T10164	kinesin heavy chai
28.5 330 2	330 2	7	7 3	ф	B48835	kinesin-like prote
813 2	813 2	7	2 T	H	46242	kinesin-like prote

	" my delightered a						
kinesin heavy chai	The state of the s	A38713	-	1031	27.3	482	
kinesin heavy chai		837711	N	1027	27.3	482	•**
kinesin-like prote		T15822	7	1584	27.3	482.5	_
kinesin-related pr		JN0114	-	1584	27.3	482.5	^1
kinesin-like prote		T40128	7	883	27.3	482.5	
kinesin-like prote		C48835	7	332	27.3	483	_
kinesin heavy chai		S44868	N	843	27.5	485.5	_
kinesin-related pr		JC5831	~	793	27.5	485.5	_
kinesin-like heavy		T51360	~	987	27.6	488	_
kinesin-related pr		S58691	٦	742	27.7	490	
kinesin heavy chai		A41919	-	963	27.8	491	
kinesin [imported]		T51932	~	929	28.0	495	_
hypothetical prote		T20621	~	928	28.0	495.5	_
kinesin [imported]		T51930	~	935	28.2	498.5	^
kinesin-like prote		A55289	ч	1150	28.3	200	_
kinesin-like spind		G02157	н	1056	28.3	501	_

ALIGNMENTS

Gaps 7 Length 665; Query Match 87.7%; Score 1550; DB 2; Length 6 Best Local Similarity 90.8%; Pred. No. 1.6e-117; Matches 314; Conservative 1; Mismatches 29; Indels

7

85 26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET ò 셤

LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNAS-VLAYGPTGAGKTHTMLGSPEQP 120 86 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNAKVVLAYGPTGAGKT-THAGQPRAT 144 62 ઠે

요

180 145 WGDPAGSHGPPAAHKGGCRGPAMGLSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGN 204 121 GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGN ઠે ద

181 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR 240 205 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR 264 ò g 241 QREGKLYLIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK 300 QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFALGKVVDALNQGLPRVPYRDSK 324 LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346 301 265 ò a ઠ

,325

T48258 kinesin-like protein - Arabidopsis thaliana N,Alternate names: protein T1E22.130



셤 g g 셤 ò 셤 셤 ਨੇ à ò ð ò ò Kinesin-related protein KLP68D - fruit fly (Drosophila melanogaster)

NyAlternate names: kinesin-like protein 5; KLP5
CiSpecies: Drosophila melanogaster
CjBate: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
CjAccession: A55236; E41298
RiPesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.
J. Cell Biol. 127, 1041-1048, 1994
A;Title: Characterization of the KuP68D kinesin-like protein in Drosophila: possible rol
A;Reference number: A55236; MUD: 95050960; PMID: 7525600
A;Recession: A55236; MUD: 95050960; PMID: 7525600
A;Residues: 1-784 <PES>
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A;Residues: 1-785 <PES C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 2000
A;Reference number: 224489
A;Reference number: 224489
A;Residue: preliminary
A;Molecule type: DNA
A;Residues: 1-64 < kBV>
A;Residues: 1-64 < kBV>
A;Residues: 1-64 < kBV>
A;Cross-references: UNIPROT: Q9LZ88; EMBL: ALI62874
A;Experimental source: cultivar Columbia; BAC clone T1E22
C;Genetics:
A;Map position: 5
A;Note: T1E22.130
A;Note: T1E22.130 FYG-ERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRAL 127 187 LIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQD 307 FYGREDDNVKHIFDREVSPLIPGIFHGFNATVLAYGATGSGKTFTMQGIDELPGLMPLTM 197 251 SVPVKŚMSEFQEAYLCGVQRRKVAHTGLNDVSSRSHGVLVISVTSQGLVT-----ĠKIN 304 68 18 ARVRVAVRLRPFV-----DGTAGASDPPCVRGMDSCSLEIANWRNHQETLK---YQFDA : ||| :|:|||: ||| : || || : || || || 3 SNVRVVLRVRPFLPREISDESCDGRSCVSVIGGDGGDTSEVAVYLKDPDSCRNESYQLDA QKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLY MDLLQLTREEGAEGRPWALSVTMSYLE1YQEKVLDLLDPASGDLV1REDCRGN1L1PGLS Length 664; 33.6%; Score 594.5; DB 2; Length 38.6%; Pred. No. 4.2e-40; Live 69; Mismatches 114; Indels SLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346 Best Local Similarity 38.69 Matches 131; Conservative 308 69 248 Query Match g 셤 셤 셤 ò ð ò ò ઠ à

P25116.11 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O: O:Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86319
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Accession: A86319
A;Status: preliminary UNIPROT: Q9FZ77; GB: AE005172; NID: g9795601; PIDN: AAF98419.1; GSPDB:GN 9 A; Description: may be part of a motor protein that provides anterograde fast ax C; Superfamily: kinesin-related protein KIF3; kinesin motor domain homology C; Keywords: AFP; coiled coil; microtubule binding; nucleotide binding; P-loop F;1-349/Domain: head globular #stetus predicted <HGIJ-F;20-350/Domain: kinesin motor domain homology <KMOT-F;106-113/Region: nucleotide-binding motif A (P-loop) F;30-580/Domain: helical rod #status predicted <HGD>F;81-84/Domain: tail globular #status predicted <HGD>F;112/Binding site: ATP (Lys) #status predicted 233 RERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP 292 70 YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD 129 58 HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L 114 5 SRRPGTGSSQTPNECVQVVVRCRPMSNRERSERSPEVVNVYPNRGV----VELQNVVDGN GSPEQPGVI PRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI 174 REDCRGN-ILIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQ 150 SRILVFVRLRPMGKKERENGSRCCVKVLNKRDVYLTEFTNENDYLRLKRLRVRHFTFDSS 12 TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN 293 HVPYRDSKLTRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYGSRAKSIQN 346 293 RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346 32; Length 784; 31.1%; Score 550; DB 2; Length 703; 38.6%; Pred. No. 1.8e-36; ive 62; Mismatches 113; Indels 18 ARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK---Indels 31.4%; Score 555.5; DB 1; 39.5%; Pred. No. 7.7e-37; tive 56; Mismatches 127; Best Local Similarity 39.5 Matches 140; Conservative Matches 130; Conservative Best Local Similarity -703 <STO> A; Molecule type: DNA A;Cross-references: C;Genetics: Query Match Query Match A;Residues: 1 ò

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A; Molecule type: DNA
A; Residues: 1-784 < PUR>
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A; Residues: 1-784 < PUR>
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A; Residues: 1-784 < PUR>
A; Residues: 1-784 < PUR>
A; Experimental source: strain 972h-; cosmid c649
R; Wood, V; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
R; Wood, V; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
A; Reference number: Z21861
A; Accession: T39531
A; Accession: T39531
A; Molecule type: DNA
A; Residues: 464-784 < WOO>
A; Cross-references: EMBL: AL031154; PIDN: CAA20063.1; GSPDB: GN00067; SPDB: SPBC1685.15c
G; Genetics:
A; Reperimental source: strain 972h-; cosmid c1685
G; Genetics:
A; Gene: SPDB: SPBC649.01c; SPDB: SPBC1685.15c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinesin-like protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: 151617; A48835; S48837
R;Vernos, I:, Raats, J:, Hirano, T:, Heasman, J:, Karsenti, E.; Wylie, C.
C;Accession: 151617
A;Title: Xklpl, a chromosomal Xenopus kinesin-like protein essential for spindle organı
A;Reference number: A56221; MUID:95236444; PMID:7720667
A;Recius: preliminary; translated from GB/EMBL/DDBJ
A;Recius: preliminary; translated from GB/EMBL/DDBJ
A;Resius: preliminary; translated from GB/EMBL/DDBJ
A;Rosius: preliminary; translated from GB/EMBL/DDBJ
A;Rosius: preliminary; translated from GB/EMBL/DDBJ
A;Rosius: preliminary; translated from GB/EMBL/DDBJ
A;Rosius: preliminary; translated from GB/EMBL/DDBJ
A;Rosius: J:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
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B;Vernos, I:, Heasman, J:, Wylle, C.
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B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Vernos, I:, Heasman, J:, Wylle, C.
B;Verno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QETL-----KYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NASVLAYGPIGAGKTHTMLGSPEQPGVI ---PRALMDLLQLTREEGAEGRPWALSVTMSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEIYQEKVLDLL--DPASGD----LVIREDCRGNILIPGLSQKPISSFADFERHFLPASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- LYLIDLAGSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 NRTMSPTEANAVSSRSHÄVLQIYITQTPKSGE-KQEESESQNSHKVRSVFSFIDLAGSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR----VPYRDSKLTRLLQDSLGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 784;
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A,Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.3%; Score 536; DB 2; Length 78
35.5%; Pred. No. 2.9e-35;
ive 61; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VRVAVRLRPFVDGTAG--ASDPPCVRGMDSCSLEIANWRNH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFROREGK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AHSILIANIAPERRFYLDTVSALNFAARSKEV 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 35.5
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
        T40594
                                                                                                                                                                                                                                                                                                                                                                                                                        A, Map position: 2
A, Introns: 11/1
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A;Residues: 1-1254 <DEH>
A;Cross-references: UNIPROT:Q94463; EMBL:U41289; NID:g1526990; PID:g1526991; PIDN:AAB077
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40594; T39531
R;Purnelle, B.; Goffeau, A.; Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, May 1998
A;Reference number: Z21939
                                                                                  189
PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR--QREGKLY 247
                                                                                                                                                                                                                                                                                                      LIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQD 307
                                                                                                                  367
                                                                                                                                                                                                                                                                                                                                     STOQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDL--- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKP 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinesin heavy chain - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                           LLQLTREEGAEGRPWALSVTMSYLETYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 30.9%; Score 547; DB 2; Length 1254; Best Local Similarity 36.3%; Pred. No. 7.2e-36; Matches 122; Conservative 76; Mismatches 126; Indels 12
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CiAccession: T18277
RideHostos, E.L.; McZaffrey, G.; Vale, R.D.
Bubmitted to the EMBL Data Library, November 1995
A;Reference number: Z18853
A;Accession: T18277
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A, Cross-references: UNIPROT: Q91785, EMBL: X94082; NID: g1129172; PID: e213754; PIDN: CAA638; C; Genetics:
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KLP2 protein - African clawed frog)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 16-Aug-2004

C;Accession: T30335

R;Boleti, H.; Karsenti, E.; Vernos, I.

Cell 84, 49-59, 1996

A;Title: XKLP2, a new Xenopus centrosomal kinesin-like protein required for centrosome

A;Reference number: Z20827; MUID:96140639; PMID:8548825

A;Accession: T30335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP-----GVIPRA--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |:: |:: | :: | : | DEDTAARGIMVRSMEDIIGGTSLD-----TDSISVSYLQLYMETIQDLLDPTNDNIAL 212
                                                                                                                                                                                                                                                                                                                    ------DQRERLAPFRQ------REGKLYLIDLAGSEDNRRTGNKGLRLKESGAIN 274
                                                                                                                                                                                                                                                                                                                                                     273 SUVENEFPUSNEMESSSHFURPSKPLVRRSKLVLVDLAGSERVHKSGSEGHMLEEAKSIN 332
                                                                                                                                                                                                                                                                                                                                                                                                                                   TSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ESVFSSVAKNIVESCANGYNGTIFAYGQTGSGKTFTMLGPSESDNFTHNLRGVIPRSFEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 LYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL----NQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 SQKPISSFADFERHFLPASRNKTVGATRINORSSRSHAVLLVKVDQRERLAPF-RQREGK
                                                                                                                                                                                                                                      20 VRVAVRLRPFVDGTAGASDPP---CVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 IKVFVRIRPPVEGTLTGVDGEQGLCLTALSSTTIRL---HSKPEPKMFTFDHVANVDTNQ
                                                                                                                                                                                                        174 REDCR-GNILIPGLSQKPISSFADPERHFLPASRNRTVGATRLNORSSRSHAVLLVKV--
                                                                                      116 SPEQP--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI
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; Pred. No. 3.2e-34;
68; Mismatches 128;
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A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: kinesin motor domain homology
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Best Local Similarity 36.5%;
Matches 126; Conservative 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNFAARSKEVIN 346
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Al, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Rieference and analysis of chromosome 1 of the plant Arabidopsis.
A; Recession: D86151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSSSASIGAADNGVPGRVRVAVRLRPRNADESVADADFADČVELQPELKRLKLRKONNW-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOODIYAGSVQPILRHILEGQNASVLAYGPTGAGKTHTMLGS-----PEQP--GVIPRAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDLLQLTREEGAEGRP-WALSVTMSYLEIYQEKVLDLLDPA---SGDLVIREDCRGNILI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR---VPYRDSK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RCRLSKIGATRRPPPARVRVAVRLRP--FVDGTAGASDPPCVR---GMDSCSLEIANWRN 57
                                                                                                                                                                                                                                                                                                                                                                                                                             74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F22M8.8 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETL----KYQFDAFYGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRVALRCRPLVP------KENNEGCKMCLIFVPGEQQVIVGTEKSFTYDYVFDPSA
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                                                                                                                                                                                                                                                                                                        30.1%; Score 532; DB 2; Length 12
36.1%; Pred. No. 1.1e-34;
ive 74; Mismatches 113; Indels
                                                                                (NCBIP:130975)
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30.0%; Score 530.5; DB 2;
Best Local Similarity 36.3%; Pred. No. 9.6e-35;
Matches 135; Conservative 66; Mismatches 132;
                                                                                                                                                                                                                                < KMOT >
                 A, Residues: 9-162,'L',164-338 <VE2>
A, Experimental source: oocyte
A, Note: sequence extracted from NCBI backbone (NCBII
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Best Local Similarity 36.1%;
Matches 125; Conservative
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Molecule type: DNA
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C;Genetics:
A;Map position: 1
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A;Introns: 56/2; 99/3; 151/3; 310/3; 343/2; 395/3; 419/1; 444/3; 462/3; 489/3; 527/1; 5
A;Note: F16L2.60
C;Superfamily: Kinesin-related protein KIP1; Kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unseld, M.; Mewes, H.W.; Rudd,
                                                                                                                                                                     141 TYTWEGGARKKNGEFPSDAGVIPRAVKQIFDILEAQGAE-----YSMKVTFLELYNEEIS 195
                                                                                                                                                                                                                                                                                                                                      173 IREDCRGNILIPGLSQKPISS----FADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                      229 KVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 LVEHLGHVPYRDSKLTRLLRDSLGGRTKTCIIATVSPAVHCLEETLSTLDYAHRAKNIRN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVL 161
                                                                        Kinesin-related protein-like - Arabidopsis thaliana
NiAlternate names: protein F1612.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47525
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W
aubmitted to the Protein Sequence Database, March 2000
A;Reference number: 224468
                                                                                                                                                                                                                                                                                                                                                                    VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRN----HOETLKYOFDAFYGERST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLSKIGATRRPPPAR----VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
  Gaps
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  44;
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Indels
                                                                                                                                            QQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS----
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A;Cross-references: UNIPROT:Q9LZU5; EMBL:AL162459
A;Experimental source: cultivar Columbia; BAC clone F16L2
Mismatches 118;
67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.6*
Best Local Similarity 33.4*
Matches 126; Conservative
131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 THIMLGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T47525
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                      186
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Matches
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A.Reference number: A84420; MUID:20083487; PMID:10617197
A.Refatus: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-1056 <STO>
A.Residues: 1-1056 <STO>
A.Greences: UNIPROT:P82266; GB:AE002093; NID:g4510356; PIDN:AAD21445.1; GSPDB:GN
                                                                                     C; Accession: T06733
R; Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigu submitted to the Protein Sequence Database, April 1999
A; Reference number: 215793
A; Accession: T0673
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable kinesin-related cytokinesis protein [imported] - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84777
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-668, 1999
                                                                                                                                                                                                                               A; Residues: 1-1070 -cQUE>
A; Residues: 1-1070 -cQUE>
A; Cross-references: UNIPROT:09SV36; EMBL:AL049655; GSPDB:GN00061; ATSP:F28P10.150
A; Experimental source: cultivar Columbia; BAC clone F28P10
C; Genetics:
A; Gene: ATSP:F28P10.150
A; Map position: 3
A; Introns: 113/2; 153/3; 194/3; 256/3; 330/3; 377/1; 427/1; 456/3; 527/3; 572/3; 632/3; C; Superfamily: kinesin-related protein KLP61F; kinesin motor domain homology
F; 124-466/Domain: kinesin motor domain homology < KWOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM--LGSPE--QPGVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCR-GNIL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKV-----DQRERLA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF-----RQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQ 289
                 inesin homolog F28P10.150 - Arabidopsis thaliana
;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARVRVAVRLRPFVDGTAGASD------PPCVRGMDSCSLEIANWRNHQETLKYQFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSSHIPTRDSKLTRLLRDSPGGSARTSLIITIGPSARYHAETTSTIMFGQRAMKIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.7%; Score 525; DB 2; Length 10
35.3%; Pred. No. 3.5e-34;
ive 69; Mismatches 120; Indels
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No. 4.1e-34;
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36.4%;
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Best Local Similarity
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A;Cross-references: UNIPROT:Q9SIB3; GB:AE002093; NID:g4580395; PIDN:AAD24373.1; GSPDB:G1
C;Genetics:
                                                                  A;Gene: At2g28620
A;Map position: 2
C;Superfamily: kinesin-related protein KIP1; kinesin motor
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29.1%;
Best Local Similarity 37:6%;
Matches 127; Conservative 63
                                                                                                                                                                                                                            Matches 122; Conservative
<STO>
                                                                                                                                                                                                    Local Similarity
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1-1076
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A; Residues:
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                                                                                                                                                                            probable kinesin-like spindle protein [imported] - Arabidopsis thaliana probable kinesin-like spindle protein [imported] - Arabidopsis thaliana (mouse-ear cress)
[C;Species: Arabidopsis thaliana (mouse-ear cress)
[C;Date: 02-Reb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
[C;Accession: B84687, R.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
[R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
[A;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
[Beuse, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
[Bature 402, 761-768, 1999
[A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
[A;Reference number: A84420; MUID:20083487; PMID:10617197
[A;Accession: B84687
[A;Accession: B84687
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[A;Accession: B8
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SGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYL 329
                       TOODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS------PEQPGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ASGDLV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 IREDCRGNILIPGLSQKPISS----FADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 KVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 LVEHLGHIPYRDSKLTRLLRDSLGGRTKTCIIATVSPAVHCLEETLSTLDYAHRAKNIKN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 VRVAVRLRPFVDGTAGASDPPCVRGMD----SCSLEIANWRNHQETLKYQFDAFYGERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: kinesin-related protein Eg5, kinesin motor domain homology, 10-361/Domain: kinesin motor domain homology <KMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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                                                                                                                          :|:| |::| |:|
376 ETLSTLDYAHRAKNIKN 392
                                                                                               DTVSALNFAARSKEVIN 346
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A;Molecule type: mRNA
A;Residues: 1-699 <COL1>
A;Cross-references: UNIPROT:P46872; EMBL:L16993; NID:g295245; PIDN:AAA16098.1; PID:g2952.
A;Accession: S72551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinesin-related protein KRPBS - sea urchin (Strongylocentrotus purpuratus)
N;Alternate names: kinesin-2 chain A; KRP (85/95) 85K chain
N;Alternate names: kinesin-2 chain A; KRP (85/95) 85K chain
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S38982; S72551
C;Accession: S38982; S72551
A;Cole, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.; Scholey, J.M.
Nature 366, 268-270, 1993
A;Title: Novel heterotimeric kinesin-related protein purified from sea urchin A;Reference number: S38982; MUID:94050179; PMID:8232586
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                                                                                                                                                                                                                                                             109
                                                                                                                                                                                                                                                                                                                          128
                                                                                                                                                                                                                                                                                                                                                                    170 QIFDILEAQSAA----EYSLKVSFLELYNEELTDLLAPEETKFADDKSKKPLALMEDGKG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RO--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEIVKSGKLNLVDLAGSENISRSGAREGRAREAGEINKSLLTLGRVINALVEHSGHIPYR 345
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                                                                                                                                                                                            20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIA---NWRNHQETLKYQFDAFYGERSTQ
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domain
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                                                          29.2%; Score 515.5; DB 2; 35.0%; Pred. No. 2.1e-33; iive 68; Mismatches 132;
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Pred. No. 1.4e-33;
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5, 2004, 18:34:12; Search time 71.0157 Seconds (without alignments): 1747.786 Million cell updates/sec
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1 MGRCRLSKIGATRRPPPARV......FYLDTVSALNFAARSKEVIN 346
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Compugen Ltd.
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GenCore version
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A_Geneseq_23Sep04:* 1: geneseqp1980s:* Database

geneseqp2001s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003bs:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

nol	Human kin		Human	_	Human	Human mic	Novel	Human kin	Human mic	Human KNS	Human pro	Drosophil	Human pro	Structura	Novel hum	Intracell	Novel hum	Human nov	Human PP	Human MDD	Novel hum	Drosophil	Candida a	Candida a	Candida a
Description	Adc23342	Adq60232	Adc23344	Adq60234	Adc23338	Adq60228	Adk40973	Adc23340	Adq60230	Adq09240	Aab56650	Abb71112	Adm04007	Ado44167	Aau76958	Abu53123	Aau76957	Adc31082	Adi15915	Abu11606	Aau76967	Abb65183	Adn40550	Adn40554	Adn40548
ΙD	ADC23342	ADQ60232	ADC23344	ADQ60234	ADC23338	ADQ60228	ADK40973	ADC23340	ADQ60230	ADQ09240	AAB56650	ABB71112	ADM04007	ADO44167	AAU76958	ABU53123	AAU76957	ADC31082	ADI15915	ABU11606	AAU76967	ABB65183	ADN40550	ADN4 0554	ADN40548
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% Query Match	100.0	100.0	100.0	100.0	99.7	99.7	99.7	7.66	7.66	7.66	99.5	•	31.6	31.6	31.2	31.2	31.2	31.2	31.2	31.2	31.1	30.3	30.1	30.1	30.1
Score	1768	1768	1768	1768	1763	1763	1763	1763	1763	1763	1753	559.5	559	559	552.5	552.5	552.5	552.5	552.5	551.5	549	535.5	532.5	532.5	532.5
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532.5 528 528	528 528 527	526 526 526 526	526 526 526 526	526 526 526 526 526 523
26 28 28	33107		33 33 40 40	44444 40640

ALIGNMENTS

RESULT 1

human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytosteratic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. Human kinesin-like DNA binding protein (KID) (SeqID 6). ADC23342 standard; protein; 346 AA. 28-NOV-2000; 2000US-00724224. 20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. (first entry) (CYTO-) CYTOKINETICS INC. WPI; 2003-706919/67. N-PSDB; ADC23341. US6387644-B1. Homo sapiens. 18-DEC-2003 14-MAY-2002. Beraud C; ADC23342; ADC23342

Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.

Claim 1, SEQ ID NO 6; 26pp; English.

systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP to phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a This invention relates to a novel method for high throughput screening

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                                                                                               This
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               as cytostatic, cardiants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer,
kinesin-like DNÀ binding protein (known as KID) as cytostatic, cardian immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. The polypeptide sequence is human KID protein (SeqID 6) of the invention.
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                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                   ; Score 1768; DB 7;
; Pred. No. 1.2e-173;
0; Mismatches 0;
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 346; Conservative
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                                                                                                                                                                                               Sequence 346 AA;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for for modulators of a mnotor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, not act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune cassociated with KID and for inhibiting KID and for treating autoimmune proliferation induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP 120
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                                                           Claim 1; SEQ ID NO 6; 26pp; English
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                       inflammation.
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Human microtubule motor protein #4.
              (first entry)
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                                                                                                                                                                                                                                                                        This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 8) of the invention.
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                                                                                                                                                                                        Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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                                                                    99US-00295612
                                                                               20-JUN-2000; 2000US-00597292
                                              28-NOV-2000; 2000US-00724224
                                                                                                      (CYTO-) CYTOKINETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                     WPI; 2003-706919/67.
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Matches 346; Conserv
                                                                                                                                                                  N-PSDB; ADC23343
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 US6387644-B1
                                                                    20-APR-1999;
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ADQ60234 standard; protein; 487 AA.

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPases activity, a method of testing for ATPases activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, or act as a modulator of the binding characteristics or biological activity of a target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restencesis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restencists, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and and of the plants of the disease and problem and protein microtubule motor protein
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Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplaaias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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Matches 346; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-532491/51
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Length 370;

Score 1763; DB 7; L Pred. No. 4.5e-173; Mismatches Score 1763;

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266 REGKLYLIDLAGSEDNRRTGNRGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 325
                                                                                                                                                                86 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                                    206 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
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                                                                       GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                             122 VIPRALMDLLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
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Query Match
Best Local Similarity 100.
Matches 345; Conservative
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                                                                                               QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK 300
                                                                                                                                                                                                                                                                                                                                                                                                              human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method for high throughput screening
                          QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                    LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                 LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                Human kinesin-like DNA binding protein (KID) (SeqID 2).
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20-JUN-2000; 2000US-00597292.
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                                                                                                                                                                                                                                                                                                                                              (first entry)
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase
                                                                                                                                                                                                                            Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
TRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2; 26pp; English.
                                                                                                                                                                                                Human microtubule motor protein #1.
                                                                                                 ADQ60228 standard; protein; 370
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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Sequence 370 AA;

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cc activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target.

Cr protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune confiseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
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Sequence 370 AA;

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                                            GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHOET
                                                        LKYQFDAFYGERSTQQD1YAGSVQP1LRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                     VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                               LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                         REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL
                        Gaps
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99.7%; Score 1763; DB 8; Length 370; 100.0%; Pred. No. 4.5e-173; cive 0; Mismatches 0; Indels C
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           Similarity
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Matches 345;
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antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia;
                                                                                                                                                                     cytostatic; immunomodulator; cardiant; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                             metabolic disorder; organ transplant rejection; enzyme
ADK40973 standard; protein; 490 AA
                                                                                                                           Novel human kinase protein #80.
                                                                                  06-MAY-2004 (first entry)
                                           ADK40973;
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and conditions to (a) and conditions to (b) perpetide in (a) except that it lacks one or more, but not all, of an CC terminal domain, a coiled-coil structure region, a spacer region and a CC terminal domain, a coiled-coil structure region, a spacer region and a CC terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or curvantal acid seases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, cor viral infections caused by fungi, ocular diseases, miltiple sclerosis, amyotrophic lateral sclerosis, viral infections caused by fungi, ocular diseases, migraines, pain, conteria, infections caused by fungi, ocular diseases, migraines, pain, conteria, infections caused by fungi, ocular diseases, migraines, pain, contesting disorders, dyskinesias, metabolic disorders and organ transplant content on invention. This sequence corresponds to one of the kinase polypeptides of the invention and corresponds to one of the kinase polypeptides of
                                                                                                                                                                                                                                                                                                                                             New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 80; 491pp; English.
                                                                                         31-DEC-2002; 2002WO-US041687
                                                                                                                                    31-DEC-2001; 2001US-0343169P
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                                                                                                                                                                                                                                                                                                                                                                                                                     metabolic disorders.
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WO2003057841-A2
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                                           17-JUL-2003
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Gaps ö Query Match 99.7%; Score 1763; DB 7; Length 490; Best Local Similarity 100.0%; Pred. No. 6.9e-173; Matches 345; Conservative 0; Mismatches 0; Indels 0

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                                                                                                                                                                                       VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
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                      34 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQET
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2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346

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Homo sapiens

87 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 146

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                                                                                                                                                                                                                                                                                                                                                                                                                         human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
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TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 378
                                                                                                                                                                                                                                                                                                                                                                  Human kinesin-like DNA binding protein (KID) (SeqID 4).
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                                                                                                                                                                          ADC23340 standard; protein; 512 AA
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20-JUN-2000; 2000US-00597292.
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N-PSDB; ADC23339.
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein act activity of a target protein, modulators of the target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac proteins useful for treating disorders and inflammation, for treating disorders
                                 206
                                                                        241
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                                                                                                                                               242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                      LIPGLSQKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                     TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 4; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microtubule motor protein #2.
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                                                                                                                                                                                                                                                                                                                                                             ADQ60230 standard; protein; 512
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET LKYQFDAFYGERSTQQDIXAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG

GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET

Best Local Similarity 100. Matches 345; Conservative

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62 27

N-PSDB; ADQ09241

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                                                                                                                                                                                                                                                                          86
associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:3, but this does not appear to be the case.
                                                                                                                                                                                                                                                                                                        LKYQFDAFYGERSTQQDIYAGSVQPILRHLLECQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                                                                                                         GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                            VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPGLSQKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                         87 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                           Length 512;
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                                                                                                                                                                                                        0; Indels
                                                                                                                                                                         99.7%; Score 1763; DB 8; L
100.0%; Pred. No. 7.4e-173;
Live 0; Mismatches 0;
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Best Local Similarity 100.
Matches 345; Conservative
                                                                                                                                          512 AA;
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Human KNSL4 protein SEQ ID NO:425. AD009240 standard; protein; 665 23-SEP-2004 (first entry) ADQ09240;

THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antianflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator; thanatos-associated protein; THAP; THAP responsive gene; THAP family; human.

(ENDO-) ENDOCUBE SAS. (CNRS) CNRS CENT NAT RECH SCI. 10-DEC-2003; 2003WO-IB006434. 10-DEC-2002; 2002US-0432699P. 03-JUL-2003; 2003US-0485027P. WO2004055050-A2 Homo sapiens. 01-JUL-2004.

Clouaire Roussigne M, Girard J, Amalric F, WPI; 2004-525034/50.

The present invention describes a method for modulating the expression of a thanaros (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-responsive gene. The method the expression of the THAP responsive gene. Also described: (1) a method of modulating the the THAP responsive gene. Also described: (1) a method of modulating the bytession of a gene responsive to a THAP/chemokine of modulating the separaceutical composition comprising a THAP responsive element; (4) a cell comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-responsive element; (1) a cell comprising a transcription factor decoy described above; (5) methods of a vector packaging cell line complex; (5) a vector packaging cell line complex; (5) a vector packaging cell line complex; (5) a vector packaging cell line complex; (5) a vector packaging cell line complex; (5) a vector packaging cell line complex; (5) a vector packaging cell which expresses a recombinant THAP-rainly polypeptide of its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-rainly polypeptide; (8) a method of mellotating cell which expresses a recombinant THAP-rainly polypeptide; (8) a method of constructing a cell comprising a viral vector which compliates the transproper of a themokine into the nucleus; (10) methods of a cancerous tissue, excessive of insufficient apoptoms; (10) methods for reducing the symptoms associated with a condition metatasis of a cancerous tissue, excessive or insufficient apoptoms; cardiovascular disease and neurodegenerative granding and a THAP-family polypeptide in an individual; (11) a vector of strainfient apoptoms; cardiovascular disease and neurodegenerative comprising a THAP-family polypeptide in an individual; (11) a vector comprising the vector described above or that expresses a THAP-family polypeptide that dees not bind to a chemokine or a THAP-family polypeptide or its Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovosacular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the Example 47; SEQ ID NO 425; 612pp; English.

GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET Gaps ö Length 665; 0; Indels 99.7%; Score 1763; DB 8; I 100.0%; Pred. No. 1.1e-172; ive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 345; Conservative ઠ

Sequence 665 AA;

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LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 145 121 181 85 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQBT LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 56 62 86 122 146 셤 a ઠ ઠે 셤

182 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 241

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                                                                                                                                                                                                                                                                                                                     Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antinfective; gynaecological; antibacterial; gone therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, grnaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive adisorders gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                266 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVFYRDSKL 325
                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences, referred to as prostate cand prevention, and diagnosis of disorders
REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                 Human prostate cancer antigen protein sequence SEQ ID NO:1228.
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Pred. No. 6.8e-172;
); Mismatches 2; Indels (
                                                                                                                         326 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                       TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
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                                                                                                                                                                                                                                                                       (first entry)
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N-PSDB; AAF15853.
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Query Match Best Local Similarity 99.4 Matches 343; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS-137-ABB-1072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                             LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                     LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                  REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                              TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 40128.
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11-JUL-2000; 2000US-00614150.
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189 187 247 305

us-10-797-893-6.rag

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detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regularing their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                               structural and cytoskeleton-associated polypeptide, SCAP, cell proliferative disorder; cancer, atherosclerosis, viral infection, HIV, neurological disorder; Parkinson's disease, Alzheimer's disease;
                                                                                                                                                                                                                                                                                                         STINAKEIMQLIMKGNRQRTQEPTAANQTSSRSHAVLQVTVRQRSRVKNILQEVRQGRLF
                                                                                                                                                                                                                                                                                19 RVRVAVRLRPF--VDGTAGAS-----DPPCVRGMDSCSLEIANWRNHQETLK-YQFDAF
                                                                                                                                                                                                                                                                                                                                                                  YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD
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95. .116
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                                                                                                                                                                                            31.6%; Score 559; DB 7;
38.9%; Pred. No. 2.8e-48;
tive 70; Mismatches 121;
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                                                                                                                                                                                                                                  58 HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L 114
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
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                                                                Length
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                                                           31.6%; Score 559.5; DB 4; 39.8%; Pred. No. 4.4e-48; ive 56; Mismatches 126;
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Seki N, Yoshikawa T,
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'note = kinesin motor domain
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'note = kinesin motor domain
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The present sequence represents a structural and cytoskeleton-associated polypeptide (SCAP). The SCAP polypeptides and polynucleotides of the invention are useful for diagnosing, preventing or treating diseases or conditions associated with aberrant expression of SCAP, such as cell proliferative disorders (e.g. cancer or atherosclerosis), viral infections (e.g. HIV) or neurological disorders (e.g. Parkinson's disease, Allahaimer's disease or stroke). These may also be used for assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are also useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. 70 YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD 129 Swarnakar A, Ho A, Hafalia AJA, Emerling BM, Ison CH, Nguyen DB; Chien D, Lu DAM, Yang YG, Yue H, Murage J, Griffin JA, Burrill JD; Wang JT, Marquis JP, Blake JJ, Chawla NK, Lee S, Becha SD, Lee SY; Richardson TW, Bhatia UG, Zheng W, Sprague WW, Tang YT, Azimzai Y; 19 RVRVAVRLRPF--VDGTAGAS-----DPPCVRGMDSCSLEIANWRNHQETLK-YQFDAF Gaps New human structural and cytoskeleton-associated proteins and polynuclectides for diagnosing, preventing or treating diseases associated with aberrant protein expression, e.g. cancer, 16; 31.6%; Score 559; DB 8; Length 998; 38.9%; Pred. No. 7.1e-48; ive 70; Mismatches 121; Indels phosphorylation site" phosphorylation site" 'note= "potential phosphorylation site" 'note= "potential phosphorylation site" "potential phosphorylation site" "potential phosphorylation site" "potential glycosylation site" phosphorylation Claim 1; Page 150-152; 205pp; English. "potential "potential "potential atherosclerosis, HIV or stroke. 27-SEP-2002; 2002US-0414227P. 18-NOV-2002; 2002US-0427594P. 07-PEB-2003; 2003US-0445724P. 07-MAR-2003; 2003US-0453277P. 24-SEP-2003; 2003WO-US030198 31.69 Best Local Similarity 38.99 Matches 132; Conservative /note= /note= /note= note= /note= 'note= (INCY-) INCYTE CORP. WPI; 2004-305155/28. N-PSDB; ADO44181. Sequence 998 AA; WO2004029205-A2 Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 08-APR-2004. 8 셤 ò g

LLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK 189

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190 PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ--REGKLY

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LIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDAL-NQGLPR-VPYRDSKLTRLL 305
                                                            248 MIDLAGSERASQTQNRGQRWKEGAHINRSLLALGNCINALSDKGSNKYINYRDSKLTRLL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel microtubule motor protein for screening modulators of HsKip3d, useful in treatment of hyperproliferative disease e.g. cancer, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease.
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//label= SwitchI motif
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//ore= "Responsible for sensing of the gamma phosphate
and initiating the conformational change between ATP and
ADP bound forms of the enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= SwitchII motif
/note= "Responsible for sensing of the gamma phosphate
and initiating the conformational change between ATP and
ADP bound forms of the enzyme"
                                                                                                                                                                                                                                                                                                                   Kinesin, motor protein; HsKip3d; cytostatic; immunosuppressive; antiarthritic; antiinflammatory; vulnerary; microtubule; inflammation; cardiac hypertrophy; cellular proliferation disease; hyperplasia; restenosis; cancer; solid tumour; cardinoma; autoimmune disease; arthitis; graft rejection; inflammatory bowel disease; surgery; angioplasty; nanotechnology; GeneChip array; expression monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Interacts with the adenine ring of ATP to form
Novel human kinesin motor protein, HsKip3d motor domain.
                                                                                             QDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 344
                                                                                                              308 KDSLGGNSRTVMIAHISPASSAFEESRNTLTYAGRAKNI 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      part of the nucleotide-binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= ATP/GTP_binding_site_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cocation/Qualifiers
                                                                                                                                                                                                AAU76958 standard; protein; 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2001; 2001WO-US024285.
                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-217176/27.
N-PSDB; ABK10348.
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                                                                                                                                                                                                                                                                                                                                                                                                              human; enzyme.
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The invention describes an isolated novel human microtubule motor protein (I) is useful for screening modulators of HsKip3d. The method comprises contacting (I) with a candidate agent in a test and control concentration, and assaying for the level of HsKip3d activity, where the HsKip3d activity between the test and control concentration indicates a modulator. A composition containing (I) is useful in the treatment of inflammation, cardiac hypertrophy, cellular proliferation diseases e.g. inflammation, cardiac hypertrophy, cellular proliferation diseases e.g. hyperplasias, reseneousls, cancer, including solid tumours of skin, breast, brain, lung, heart, bone, genitourinary tract, liver, nervous system, adrenal glands, haematologic, gynaecological and testicular carcinomas, autofimmune disease, arthritis, graft rejection, inflammatory bowel disease, proliferation induced after medical procedures, such as surgery, angioplasty. The motor domains may also be used in nanotechnological applications, and polymuclectides encoding the proteins is further useful for inclusion on GeneChip (RTM) array or for use in expression monitoring. This is the amino acid sequence of the novel human motor inclusion contents of the motor domain, the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.2%; Score 552.5; DB 5; Length : Best Local Similarity 39.7%; Pred. No. 6.9e-48; Matches 141; Conservative 59; Mismatches 114; Indels
Claim 11; Fig 3; 66pp; English.
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Best Local Similarity
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US-09-724-224-5
US-09-724-224-5
Sequence 5, Application US/09724224
Fatent No. 6387644
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 638764el motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: US/09/724,224
FRIOR APPLICATION NUMBER: US/09/724,224
FRIOR APPLICATION NUMBER: 2000-620
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1041
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US-09-967-908A-3
US-09-967-908A-1
US-09-967-908A-1
US-09-967-908A-1
US-09-967-908A-1
US-09-724-511-1
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US-09-724-511-1
US-09-724-511-1
US-09-723-344-1
US-09-723-344-1
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100.0%; Pred. No. 0;
cive 0; Mismatches
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; ORGANISM: Human
US-09-724-224-5
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ATTGCCCCTGAGAGGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCGGG 1020
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                                                                                                                                   GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG 900
                   721 CAGCGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGGGCACA
                                                                                      GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCTG
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                                                                 GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCTCCTGTTTGTCCTG
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; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use; FILE REFERENCE: 104.
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; NUMBER OF SEQ ID NOS: 8
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1039; Conservative
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TYPE: DNA
ORGANISM: Human
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                   Sequence 7, Application US/09724224

Fatent No. 6387644

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: No. 6387644el motor proteins and methods for TITLE OF INVENTION: their use

FILE REPERRNCE: 1044

CURRENT APPLICATION NUMBER: US/09/724,224

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION WHERE: 09/597,292

PRIOR APPLICATION WHERE: 09/597,292

PRIOR PLING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 1464
                                                                                                                                                                                                                                                                                                                                                              Query Match 99.8%; Score 1038.4; DB 3; Length 1464; Best Local Similarity 99.9%; Pred. No. 0; Matches 1039; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 4 GGCGTGTCGGCTAAGCAAGATTGGAGCTACTCGTCCTCCACCTCCACTCGCGTAAGG 6 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	198 GTGCGGGGCATGGACCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT 2 184 CTCAAATACCAGTTTGATGCCTTCTATGGGGACGAGGACTACTAGGACACTATGCA 2	318 GGTTCAGTGCAGCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC 3 304 TATGGACCCAAGAGCTGGGAAGACGCACACACAGGCAGCCAGAGCAACCTGGG 3 105 TATGGACCCACAGGAGCTGGGAAGACGCACACACACAGGAAGCAGCCAGAGCAACCTGGG 3 364 GTGATCCCGCGGGCTCTCATGGACCTCCTGCAACTCAAAGGAAGAAGAGAGGAGCCAGAGCCAGAGCCAGAGCAACTTGGA 4 364 GTGATCCCGCGGGCTCTCATGGACCTCCTGCAGACAAGAGAAGAAGAAGAGAGAG	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 8 4 8 4	558 544 618 604	678 664 738	724 CGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC 	2y 784 AACAAGGGCCTTCGGCTAAAAGAGAGGGGGCATCAACACCCTCCTGTTTGTCCTGGGC 843	29 844 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCTCGTGTACCTTATCGGGACAGCAAGCTC 903	2y 904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963	2y 964 GCCCTGAGAGACGCTTCTACCTAGACACACTCCGCACTCAACTTTGCTGCCAGGTCC 1023	2y 1024 AAGGAGGTGATCAATTGA 1041
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738 AGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAG 797

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1038 GCCCTGAGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 1097
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                                                                                            858 AACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCCCCTTTGTCTCTGGGC 917
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                                   798 CGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC
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   CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCGCACAGGC
                                                                                                                                             AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCTC
                                                                                                                                                                                                                   ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT
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Patent No. 6387644

GRERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION: their use
CURRENT PAPLICATION NUMBER: US/09/724,224

CURRENT APPLICATION NUMBER: 09/597,229

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR FILING DATE: 2000-06-20
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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100.0%; Pred. No. v.
                                                                               TITLE OF INVENTION: No. 6762043el motor prot
TITLE OF INVENTION: No. 6762043el motor prot
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/093,317
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/724,224
PRIOR FILING DATE: 2000-11-28
WUMBER OF SEQ ID NOS: 8
SOFTWARE: FASESEQ for Windows Version 4.0
                              Sequence 1, Application US/10093317
Patent No. 6762043
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 1038; Conservative
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ORGANISM: Human
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LENGTH: 1115
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Query Match 99.5%; Score 1035.4; DB 4; Length 1538; Best Local Similarity 99.9%; Pred. No. 9.9e-315; Matches 1036; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 4 GGTCGCTGCTGCTGCTAAGCAAGCTAACGAGCTACTCGTCGTCGACTCCAGCTCCAGCTAAGG 63 Db 78 GGTCGCTGTCGGCTAAGCAAGCTAAGAGCTACTCGTCGTCCACCTCCAGCTCCGCGTAAAGG 137	64 GTGGCTGTGCGCCATTTGTGGATGGACAGCGGAGCAAGTGATCCCCCCTGT 138 GTGGCTGTGCGGCCATTTGTGGATGGACAGCGGAGCAAGTGATCCCCCCTGT 124 GTGCGGGGCATGCGGCCATTTGTGGATGGAACAGCGGAGGAACCACGCTGT 125 GTGCGGGGCATGGACGCTCTCTAGAGATTGCTAACTGGAGGAACCACGGGAGACT 198 GTGCGGGGCATGGACGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACGGGAGACT 198 GTGCGGGGCATGGACACCTCTCTAGAGATTGCTAACTGGAGGAACCACGGGAGACT	Qy 184 CTCAAATACCAGTTGATGCCTTCTATGGGGAGAGTACTCAGCAGCACTCTATGCA 243 Db 258 CTCAAATACCAGTTTGATGCCTTCTATGGGAGAGAGACTCTCAGCAGCACTCTATGCA 317 Qy 244 GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCCAGAATGCCAGTGCTTGCC 303 Db 318 GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCCAGAATGCCAGTGTGCTTGCC 377 Qy 304 TATGGACCCACCATCCTAAGGCACTACACAATGCTGGAGAGCCAGAATGCCTTGCC 377		Db GGCCATGGCCTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAATTA 557 Qy GACCTCCTGGCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGGGGGGAATATC 543 Db S58 GACCTCCTGGATGGTTGGGAGAACTGGTAATCCGAGAGAATATC 543	Qy 544 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC 603 b 618 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC 677 Qy 604 CTGCCAGCCAGTCGAAATCGGAACGCTGAAGGAGCCCCCGGGCTCCAACGGCTCCTCCCGC 663	Db 678 CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGCTCAACCAGCGCTCCTCCCGC 737 Qy 664 AGTCATGCTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAG 723 Db 738 AGTCATGCTGTGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAG 797	Qy 724 CGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACGGCGCACAGGC 783 Db 798 CGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC 857	OY 784 AACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCCCTGTTTGTCCTGGGC 843	Oy 844 AAAGTGGTAGATGGCCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAGGACGCGGGACAGCAAGCA	Qy 904 ACTGGCCTATTGCAGGACTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963	Oy 964 GCCCTGAGAGGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 1023
	424 CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAGAGTATTA 483 [CTGCCAGCTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTTTGCTGATTTTTGAGCGGCACTTC CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCCAACCAGCGCTCCTCCCGC	CGAGAGGGAAAACTCTACCTGATGACTGGGTGGGGTCGGGGAAACGTTTGGCCCCATTTCGGTGGGGTCGGGGGAAACGCCCCGGGCGCGCGC	AACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGC AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAGCTC	904 ACTGGCCTATTGCAGGACTCTCTGGGTGGCTCAGGATATCCTTATTGCCAACATT 963	AAGGAGGTGATCAATTG 1040 	ULT 8 10-093-317-3 equence 3, Application US/10093317 arent No. 6765043	NEEL INFORMATION: PPLICANT: Beraud, Christophe TITLE OF INVENTION: No. 6762043el motor proteins and methods for	TILE CE ANYENTEUR: CHELL USE TILE REPERENCE: 1044 UNRENT APPLICATION NUMBER: US/10/093,317 UNRENT FILING DATE: 2002-09-06-06-06-06-06-06-06-06-06-06-06-06-06-	PRIOR FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0	LENGTH: 1538 TYPE: DNA ORGANISM: Human

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ORGANISM: Human
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Pred. No. 2.4e-32;
0; Mismatches 389;
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ORGANISM: Artificial Sequence
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Best Local Similarity 51.2%;
Matches 437; Conservative
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APPLICANT: Davies, Katherine A.
IITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR I FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
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Patent No. 6680369
GENERAL INFORMATION
APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew
APPLICANT: Yu, Ming
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Patent No. 638841

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

APPLICANT: Breadnan, Richard

TITLE OF INVENTION: No. 6368841e1 motor proteins and methods for TITLE OF INVENTION: their use

FILE REFERENCE: 1045

CURRENT FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: US/05/21,233

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PRESENCE of IN Windows Version 4.0
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Best Local Similarity 50.1%; Pred. No. 5.9e-30;
Matches 429; Conservative 0; Mismatches 356; Indels
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NAME/KEY: misc feature
LOCATION: (472)... (495)
OTHER INFORMATION: n = a, c, t, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1024 AAGGAGGTGATCAATTG 1040
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ORGANISM: Human
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                                                                                                                                                                                           Sequence 1, Application US/09621233
Patent No. 6294371
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6294371e1 motor proteins and methods for
TITLE OF INVENTION: their use
FILE REPERENCE: 1045
CURRENT APPLICATION NUMBER: US/09/621,233
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 4.0
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OTHER INFORMATION: n = a, c, t, or g
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 897
                                                                                                                                                                    -09-621-233-1
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US-09-621-233-1
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                                                                                    CCCACAGGAGCTGGGAAGACGCACACATGCTGGGCAGCCCAGAGCAACCTGGGGGTGATC
                                                                                                                                                                                             CCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCCTGCCA
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Fatent No. 6391573
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6391573e1 motor proteins and methods for
TITLE OF INVENTION: No. 6391573e1 motor proteins and methods for
TITLE OF INVENTION: No. 6391573e1
FILE REFERENCE: 1045
CURRENT APPLICATION NUMBER: US/09/724,516
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/621,233
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (472)...(495)
OTHER INFORMATION: n = a,
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US-09-724-516-1
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                                                                                                                                                                                          Gaps
                                                                                                                                                      Score 127.8; DB 4; Length 897;
Pred. No. 5.9e-30;
0; Mismatches 356; Indels 72;
                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (472)...(495)
COTHER INFORMATION: n = a, c, t, or g
US-10-090-695-1
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                                                                                                                                                      Query Match
Best Local Similarity 50.1%;
Matches 429; Conservative 0
            TYPE: DNA
ORGANISM: Human
LENGTH: 897
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: November 9, 2004, 19:47:28; Search time 4600.34 Seconds (without alignments) 10701.074 Million cell updates/sec Title: US-10-797-893-5 Perfect score: 1041 Sequence: 1 atgggtcgctgtcggctaagccaaggaggtgatcaattga 1041 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 4526729 segs, 23644849745 residues Total number of hits satisfying chosen parameters: 9053458 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 04	seting first engmbl:* gb_htg:* gb_ntg:* gb_on:* gb_ov:* gb_pt:* gb_pt:* gb_pt:* gb_pt:* gb_rt:* gb_rt:* gb_v:* gb_v:* gb_v:* gb_v:* gb_v:* gb_v:* gb_v:* gb_v:* gb_v:*	No. Score Match Length DB ID Description

ORIGIN Query Match 99:8%; Score 1038.4; DB 6; Length 1464; Best Local Similarity 99.9%; Pred. No. 9.5e-267; Matches 1039; Conservative 0; Mismatches 1; Indels 0; Gaps 0	Qy 1 AIGGGTGGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCGTCCTCCAGCTCGCGTA 60	QY 61 AGGGTGGCTGTGCGGCCATTTGTGGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	Oy 121 TGTGTGGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAG 180	QY 181 ACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGAGTACTCAGGAGACATCTAT 240	Oy 241 GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCCAGAATGCCAGTGTGCTT 300 241 GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCCAGAATGCCAGTGTGCTT 300	QY 301 GCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCT 360 Db 301 GCCTATGGACCCACAGGAGCTGGGAAGACGCACAATGCTGGGCAGCCCAGAGCAACT 360	QY 36.1 GGGGTGATCCCGCGGGGTTCTCATGGACCTCCTGCAGGTGCCGAGGGGTGCCGAGGGTGCCGAGGGTGCCGAGGGTGCCGAGGGTGCCGAGGGGTGCCGAGGGGTGCCGAGGGGGTGCCGAGGGGGTGCCGAGGGGGGTGCCGAGGAGGGGGGGG	Qy 421 GGCCGGCCATGGCCCTTTCTGTCCATGTCTTACCTAGAGATCTACCGGAGAAGGTA 480	QY 481 TTAGACCTCCTGGTCTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGAAT 540	QY 541 ATCCTGATTCCGGGTCTCTCCCAGAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCAC 600 L	Oy 601 TTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCC 660	QY 661 CGCAGTCATGCTGTGCTCCTGGTCGACCAGGGGAACGTTTGGCCCCATTTCGC 720	09 721 CAGCGAGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCACA 780	841 GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG	Oy 901 CTCACTCGCCTATTGCAGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC 960	OY 961 ATTGCCCTGAGAGGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGG 1020
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	9.58 9.18 9.04 9.78 9.64		137 AR210053 137 LOCUS 123 LOCUS 123 ACCESION VERSION 197 KENWORDS	183 257 243 317	303 Source 377 ORIGIN	GGG 363 Query Match 99.5%; Score 1035.4; DB 6; Length 153 Best Local Similarity 99.9%; Pred. No. 6.1e-266; GGG 437 Matches 1036; Conservative 0; Mismatches 1; Indels 0	GGC 423 Qy	TTA 483 Oy 64 GIGGCIGTGCGACTGCGGCCATTTGTGGAAGGGGGGGAGCAGTGAITCCCCCCTGT	ATC 543 QY 124 GTGCGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT	TTC 603 Qy 184 CTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGAGTACTCAGCAGGACATCTATGCA	CGC 663 OV 244 GGTTFCAGGCCCATTCTABAGGCAATGCAAAAGCAAAAAAAAAAA
linear PAT 20-	Unknown. Unknown. Unclassified. 1 (bases 1 to 1115) Beraud,C. Motor proteins and methods for their use Patent: US 6387644-A 1 14-MAY-2002; Location/Qualifiers 1115 /organism="unknown" /mol_type="unassigned DNA"	T.		GTGCGGGGCATGGACGCTGCTCTAGAGATTGCTAACTGGAGAACCACCAGGAGACT [GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC 	TATGGACCCACAGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG 	GTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCAAGGGAGGAGGAGGGTGCCGAGGGC 	CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA	GACCTCCTGGACCTGCTTCGGGAGACCTGGTAATCCGAGAGAGTGCCGGGGGAATATC	CTGATTCCGGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC	CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGC

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Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and Hindill sites of the pDNN-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATC' to provide Kozak consensus sequence; 'GG' after last codon and before Hindill site to maintain reading frame. Location/Qualifiers
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARV
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GSEDNRRTGWKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLG
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LLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLDRLL
ASQCSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAEEKENHC
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EPBEKAEDCWELQISPELLAHGRQKILDLINEGSARDLRSLQRIGPKKAQLIVGWREL
HGPPSQVEDLERVEGITGKQMESFLKANILGLAAGQRCGAS"
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                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG
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/note="Vector: pDNR-Dual"
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Pred. No. 6.1e-266;
0; Mismatches 1;
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1 (Dases 1 to 1998)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundânya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Chen,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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Homo sapiens kinesin-like 4 mRNA, complete cds.
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BPEEKARDGWELQISPELAHGRQKILDLLNEGSARDLRSLQRIGPKKAQLIVGWREL
HGPFSQVEDLERVEGITGKQMESFLKANILGLAAGGRCGASL"
This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Bed, CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and Hiddlin sites of the PDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before Hiddli site to maintain reading frame. Location/Qualifiers
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/note="Mutations: 1997:Stop->Leu"
                                                                                                                                                                                                                                                                                                                                              /lab_host="DH5alpha T1 resistant"
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Pred. No. 6.1e-266;
0; Mismatches 1;
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collection"
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Br007888
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synthetic construct
synthetic construct
sartificial sequences.
1 (bases 1 to 1998)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundiny, and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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(bases 1 to 1998)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalnine,N., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
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424 CGGCCATGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA 496 CGCCATGGCCCTTTCTTCTCTCCCTAGAGATCTACCAGGAGAAGGTATTA 496 CGCCATGGCCCTTTCTGCCACTCTTACCTAGAGATCTACCAGGAGAAGGTATTA 484 GACCTCCTGGACCCTGCTTCGGGAGACCTGTACCGAGAAGATTTC 556 GACTCCTGGACCTTCGGGAGACCTGGTAATCCGAGAAGATTTC 577 CTGATTCCGGGCCTTCCCCAGAAGCCTAGTAGCTTTGCTGCTGCGGGGGAATATC 616 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC 617 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTTGAGCGGCACTTC 618 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTTGAGCGGCACTTC 619 CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCCACCGGCCCCCCCGGCCCCCCCGGCCCCCCCGGCCCCCC	Db 736 AGTCATGCTGGTCAAGGTGGACCAGCGGAAACGTTTGGCCCATTTCGCCAG 795	904 ACTCGCCTATTGCAGGCTCTCTGGGTGCCCCCTATTGCCACATT 904 ACTCGCCTATTGCAGGCTCTCTGGGTGCCCCCAGTATCCTTATTGCCACATT 976 ACTCGCCTATTGCAGGCTCTCTGGGTGCTCCAGCTCTCTTTTGCCACATT 964 GCCCTGAGAGCTCTCTCTGGGTGCTCTCGCCCCCCACATTTGCTGCTGCCAGTCC 1036 GCCCTGAGAGCTTCTACCTAGACACATTTCTTGCTGCCAGGTCC 1024 AAGGAGGTGATCATTGCTAGCTGCCAGACTCTCCGCCACTCACT	RESULT 7 AR304057 LOCUS DEFINITION Sequence 34 from patent US 6544766. DEFINITION Sequence 34 from patent US 6544766. ACCESSION Sequence 34 from patent US 6544766. ACCESSION AR304057.1 GI:31692955 KEYWORDS SOUNCE ONGANISM Unknown. Unclassified. Unclassified. Unclassified. 1 (bases 1 to 2097) AUTHORS Beraud,C., Ohashi,C., Sakowicz,R., Vaisberg,E., Wood,K. and Yu,M. AUTHORS Human kinesins and methods of producing and purifying human JOURNAL Patent: US 6544766-A 34 08-APR-2003; FRATURES 1. 2097 Authors Source Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Analysis Authors Accession Analysis Authors Accession Analysis Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Authors Accession Analysis Analysis Authors Accession Analysis Analysis Analysis Analysis Analysis Analysis Analysis Analysis Analysis Analysis Accession Analysis An	Okigin Query Match Query Match Query Match Best Local Similarity 99.5%; Score 1035.4; DB 6; Length 2097; Best Local Similarity 99.9%; Pred. No. 6.1e-266; Matches 1036; Conservative 0; Mismatches 4 GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCCTCCTCCTCCACTCCGCGTAAGG Dy

us-10-797-893-5.rge

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7 bp mRNA linear PRI 29-JUN-2004
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                          GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC
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Tokai-Nishizumi, N. and Edamasu, M.

Tokai-Nishizumi, N. and Edamasu, M.

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(E-mail:tokai@hgc.ims.u-tokyo.ac.jp, Tel:03-5449-5302,

Fax:03-5449-5413)

D38751:Submitted (02-Nov-1994)

Sequence updated (25-Feb-1999).

Location/Qualifiers

Location/Qualifiers

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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
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for kinesin-like DNA binding protein, complete
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220 GTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT
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Kid, a novel kinesin-like DNA binding protein, is localized chromosomes and the mitotic spindle
EMBO J. 15 (3), 457-467 (1996)
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                                                        AB017430.2 GI:4519442
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Momo sapiens (human)
Homo sapiens
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25. .2022
  sapiens mRNA
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             Straubberg A.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Rkhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 62 Row: 1 Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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SEDRRRTGARGLKESGALNTSLEVLGKVVDALNGSLPRVPYRDSLTRLLDDSLG
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EPERKAEDWELQISPELLAHGROKILDLANEGSARDLKSLORIGPKKAQLIVGWREL
HGPPSQVEDLERVEGITGKOMESPLKANILGIAAAGORGAS!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 GIGCGGGGALGGACACTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGATTCCGGGTCTCTCCCCGGAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGAGTACTCAGCAGGACATCTATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGATCCCGCGGGGCTCTCTATGGACCTCCTGCAGCTCACAAGGGAGGAGGGTGCCGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCCAGGAGAAGGTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               561 GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGGAATATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%; Score 1035.4; DB 9; Length 2117; 99.9%; Pred. No. 6.1e-266; ative 0; Mismatches 1; Indels 0;
  member 22"
/product="kinesin family
/protein_id="AAH28155.1"
/db_xref="G1:20380447"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: f Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADFERHFLPASRNRTVGATRLMQRSSRSHAVILVKVDORERLAPFRQREGKLYLIDLA
SESDRRATGRICKLKESGALNTSLEVLGKVVDALDAGGEPPYPROSKITRLLQDSLG
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EPEEKABOCNELQISPELLAHGRQKILDLINGGSARDLESLGY
                             info@bcgsc.bc.cs
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petreecu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="gynonyma: KID, OBP, OBP-1, OBP-2, KNSL4"

db_xref="LocuaID:3835"

/db_xref="MIM:603213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1035.4; DB 9; Length 2134;
Pred. No: 6.1e-266;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Lung, small cell carcinoma"
/clone_lib="NIH MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        member 22'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="MGC:1573 IMAGE:3535435"
          BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="kinesin_family
/protein_id="AAH04352.1"
/db_xref="GI:13279308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism≂"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="KIF22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="KIF22"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   1023
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22, mRNA (cDNA clone MGC:1573
                                                                                   843
                                                                                                                                       920
                                                                                                                                                                                        903
                                                                                                                                                                                                                                           980
                                                                                                                                                                                                                                                                                               963
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
AACAAGGCCTTCGGCTAAAAGAGAGAGCGATCAACAACACCTCCCTGTTTGTCCTGGGC
                                                                                                                                                                                                                     921 AAAGTGGTAGATGCGCTGAATCAGGCCTCCCTCGTGTACCTTATCGGGACAGCACAGCTC
                                                                                                                                                                                                                                                                                         ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
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Homo sapiens kinesin family member
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/translation="MSLRAKTCPQRREMASATSGPGRCVSKGGLGRRPPLARVRVAVR
LRPPMDGETEAKELPCVRAIDSCSLEVANWKKYQETLKYQFDAFYGEKSTQQEVYYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: m Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21704181.
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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/protein id=AAH03427.1"
/db_xref="GI:13097360"
/db_xref="LocusID:110033"
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/clone="MGC:6456 IMAGE:2615715"
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/db_xref="LocusID:110033"
/db_xref="MGI:109233"
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/strain="FVB/N"
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ander, E., Ali, A., Allen, N., Chang, J., Chazaro, B., Chang, J., Chazaro, B., Chang, J., Chazaro, B., Collymore, A., Cook, A., Diaz, J.S., Dodge, S., Faro, S., Salagan, J., Gardyne, S., am, L., Grand-Pierre, N., Iliev, I. Liu, G., Lakocque, K., Lu, C., Lakocque, K., Lu, C., Lakocque, K., Marthews, C., Marquis, N., Matthews, C., Mcquis, N., Matthews, C., Phy, T., Naylor, J., Nguyen, C., O'Donnell, P., O'Neil, D., Pierre, N., Pollara, V., Perre, N., Pollara, V., Perre, N., Pollara, V., Rise, C., Schauer, S., Schupback, R., ange-Thomann, N., Stojanovic, N., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, S., Theodore, J., Tesfaye, N., Tourg, G., Ye, W.J., Young, G., ouelleil, A., Allen, N.,
Bastien, V., Bloom, T.,
Tata, J., Chang, J., Choepel, Y.,
Tata, J., Extellano, K.,
Ts.L., Erickson, J., Faro, S.,
Galagan, J., Gardyna, S.,
Hagopian, D., Hagos, B.,
I., Johnson, R., Jones, C.,
I., Johnson, R.,
Matthews, C., McCarthy, M.,
Matthews, C., McCarthy, T., Naylor, J.,
Honkhang, P., Pierre, N., ACAGTATCCTTATTGCCAACATTGC 965 ACTCAACTTTGCTGCCAGGTCCAA 1025 linear HTG 14-MAR-2003 DRAFT SEQUENCE, 4 unordered 1; Vertebrata; Euteleostomi; lathi; Muridae; Mus. itute/MIT Center for Genome e, MA 02141, USA

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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518 33617: gap of 100 bp

6618 42736: contig of 9119 bp in length

42836: gap of 100 bp

8837 84394: contig of 41558 bp in length

885 84494: gap of 100 bp

685 151041: contig of 66547 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                       Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L17745
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Best Local Similarity 80.0%; Pred. No. 2.8e-170;
Matches 824; Conservative 0; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment
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33618. .42736
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Johnson, R., Jones, C., Kamar, A., Kartas, A., Kells, C., Landers, I., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngywen, C., Ngywen, T., Nicol, R., Norbu, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Endyer, P., Romon, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo.A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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1. 1655
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         fagopian, D., Hagos, B., Hall, J., Horton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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/rpt_family="AT_rich"
2115. .2157
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1202. .4363
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1000. .4180
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complement(8512..859
/rpt_family="MLT11"
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605. .3666
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8445. .8509
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Direct Submission

Submitted (13-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 164759)

Birren, B., Wusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, C., Chang, J., Choepel, Y., Cook, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzderald, M., Gadgan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Hafez, V., Matchews, C., Mocarthy, M., Macdonald, P., Major, J., Manthews, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Madow, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, B., Stange-Thomann, W., Schupback, M., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Wasiliev, H., Vorhaz, T., Sember, M., Wilson, B., Wu, X., Wymann, D., Young, G., Zainnoun, V., Zembek, L., Zimmer, A. and Zody, M., Direct, Submission
                                                                  AC101752 164759 bp DNA linear ROD 23-APR-2004
Mus musculus chromosome 1, clone RP24-344C18, complete seguence.
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Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choppel,Y., Collymore,A., Cook,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Raro,S., Ferreixa,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mus musculus chromosome 1, clone RP24-344C18
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145871 ACAGCCCATACTAAGGAACTTGCTGGAAGGGCAGAGATGCCAGTGTACTTGCCTATGGACC 145812
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HTG; HTGS_PHASE1; HTGS_FULTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
               145931 TCAGTTTGATGCCTTCCATGGAGAAGAAGACCACTCAGTGGGACATCTATGTAGGTTTAGT
                                                                                                                              CTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCCAACTTTGCTGCCAGGTCCAAGG
                                                                                                                                                                       GGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAGACCTCCT
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                                                                                                               CACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGTGATCCC
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complement (18235. .18777)
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complement(36134. .36736)
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complement(11397..17527
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21799. .21907
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inis record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                     15450: contrig of 80458 bp in length 15450: gap of 100 bp 167808: contrig of 100 bp 167808: contrig of 1358 bp in length 167808: contrig of 1358 bp in length 16791: contrig of 8803 bp in length 176711: contrig of 8803 bp in length 176712: contrig of 5689 bp in length 1501 233500: contrig of 5689 bp in length 1601 233500: gap of 100 bp 1660 241222: contrig of 7622 bp in length 1623 297639: contrig of 56317 bp in length 16023 297639: contrig of 56317 bp in length.
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                                                                                            contig of 63747 bp in length gap of 100 bp contig of 10045 bp in length gap of 100 bp
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/clone_lib="RPCI-24 Male Mouse BAC"
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                                                                                                                                               Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Delxellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Gorde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamdersters, R., Landerster, T., Lehoczky, J., Levine, R., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., Mropheters, R., Meldrim, J., Meneus, L., Mihova, T., Major, J., Marquis, N., Matthews, C., Norman, C.H., McKernan, R., Morbie, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Najor, J., Sebuer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stanges, Topham, K., Travers, M., Travis, N., Trajilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., and Zody, M., Submission.
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Burnited (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Sa (bases 1 to 297639)

Birren, B., Nusbaum, C., Lander E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boqualavkiy, L., Boukhgalter, B., Canarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Collymore, A., Cooke, P., Coley, K., Doris, L., Erickson, J., Farro, S., Ferreira, P., Fitckerid, M., Gage, D., Galagan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Madonald, P., Major, J., Manning, J., Matthews, C., Macdonald, P., Major, J., Mahova, T., Mienga, V., Wurphy, T., Naylor, J., Manol, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojamovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wwman, D., Young, G., Zainoun, J., Zembek, L., Direct Submission

All prepars were identified using Repearablasker:

All repeats were identified using Repearablasker:
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Center: Whitehead Institute/MIT Center for Genome Research
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------ Project Information
Center project name: L17732
                                         irren,B., Nusbaum,C. and Lander,B.
us musculus chromosome 1, clone RP24-275J1
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Gaps

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Biren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Chang, J., Erickson, J., Farco, S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farro, S., Ferraira, P., Strad-Pierre, N., Hafez, N., Hafez, N., Hagoplan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kame, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Nei, D., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stenan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stohanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassalliev, H., Vonkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M., Khien, B., Wu, S., Willer, M., Subbis, M., Talamas, J., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 1, 2004 this sequence version replaced gi:46358225.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Research, 320 Charles Street, Cambridge, MA 02141, USA
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Contact: sequence_submissions@broad.mit.edu
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/organism="Mus musculus"
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Center clone name: 202 A 19
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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
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Mus musculus chromosome 1, clone RP23-202A19, complete sequence.
AC102127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 CTGAAAGATGTTTTTACCTGGATACAATCTCAGCATTAAACTTCACTGCTAGGTCCAAGG 162
                                                                                                                                                                                                                                                                                           AAAACTCTACCTTATTGATTTGGCTGGTTCAGAGGACAACCGTCAGTCGCACGAGGAACC 402
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 196674)
                                       CAGTAGAAATCGAGTTGTAGGAGCTACTCTGCTTAACCAGCGCTCTTGCCGTAGTCATGC
      CAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGCAGTCATGC
                                                                                                                   672 TGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCGAGGGG
                                                                                                                                                                          521 AGCGCTCTTGGTCAAGGTAGATCAGCATGAACGTTTGACTCCATTTCGCCAGTGGGAAGG
                                                                                                                                                                                                                                       AAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACC----GGCGCACAGGCAACA
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Mus musculus chromosome 1, clone RP23-202A19
Unpublished
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.208. .1291
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complement (9243. .9815)
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complement(1974. 2067)
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101632 TTTATGACTATGCCCCATTTATGGATGAAAAAAAGGAAAGGAAAGGATGCCCTTGTGTAAG 101691
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102349 ACCAGTGCATTCAACTCAAAGAGAGTGGCGCCATCAACAACCT-GCTTCTTGTACTGGGCA 102407
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                                                                       Complement (1608. . 16517)

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16809. . 16866

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Abes7215 Human kin Adj9507 Novel NOV Aa19619 BUNA encod Adm81051 Human Hsk Abc40796 Toxicity Abc40796 Toxicity Abd73061 Human kin Aa156806 DNA encod Adb66785 DNA encod Abd673062 Human kin Aa156807 DNA encod Adb66787 DNA encod Adb66787 DNA encod Adb6787 Bunan nov Adc30569 Human nov Adc30569 Human nov Adc30569 Human NOV Adc30569 Human NOV Adc30569 Human kin Adc10189 Human kin Adc10189 Human kin Adc10189 Human kin Adc10189 Human kin Adc10189 Human kin Adc10189 Human kin Adc10189 Human kin Adc10189 Human kin Adc10189 Human bon Abl28591 Human bon Abl88681 Human bon Abl886911 Human bon

ALIGNMENTS

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DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 5).
                                                                                                                                                                                                                                                                                                                                     human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.

    1041
/*tag= a
/product= "KID protein"

                                 ADM81051
ABT40796
ABC73061
AAL56806
ADB66785
ABG73062
AAL56807
ADB66787
ADB66787
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ABB94615
                                                                                                            ADC30338
ADC30569
ABL16733
AAD28568
ADC10189
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AAD28569
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                                                                                                                                                                                                                                                                    ADC23341 standard; DNA; 1041 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
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                                         WPI; 2003-706919/67.
P-PSDB; ADC23342.
11.0
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136.6
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127.8
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RESULT
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Adc60231 Human mic
Adc2333 DNA encod
Adc60233 Human mic
Adc2333 DNA encod
Adc60227 Human mic
Adc60227 Human mic
Add60229 Human mic
Add60229 Human pic
Adx40995 Novel hum
Aaf15853 Human foe
Ach71408 Human gen
Ach71408 Human gen
Ach91108 Human gen
Ach91108 Human gen
Adm1564 Human gen
Adm1564 Human gen
Adm1564 Human gen
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Adv4181 DNA encod
Ady4181 DNA encod
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Adj95073 Novel NOV
Abx34596 Human mdd
Aba97216 DNA encod
Aba97216 DNA encod
Aba94614 Human kin
                                                       ; Search time 538.26 Seconds
(without alignments)
10152.424 Million cell updates/sec
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                                                                                                           1 atgggtcgctgtcggctaag.........
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                                                                                                                                                                       8269772
       5.1.6
Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                    4134886 segs, 2624710521 residues
      GenCore version
Copyright (c) 1993 - 2004
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                                                        9, 2004, 09:45:10
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Maximum Match 100%
Listing first 45 summaries
                                       - nucleic search, using sw model
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ADQ60227
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ABA94616
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ABA94614
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Gapop 10.0 , Gapext 1.0
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consistency invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are appale of modulating the activity of target proteins having motor compains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using considerable that identifies modulators of the target protein, which is a method that identifies modulators of the target protein, which is a considerable immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, cardiants hypertrophy, immune disorders and inflammation. This polymucleotide sequence is human KID DNA (SeqID 5) encoding a full length can be uncention.
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                                                                     GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG
                                                                                                                                     CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC
                                                                                                                                                                 ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGGTCTCCGCACTCCAACTTTGCTGCTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                        GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG
                                                       GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG
                                                                                                          CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC
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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using
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                                                                                                                                                                                                                                                                                                                                                             proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune chiseased, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubule motor protein of the invention.
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Pred. No. 5e-296;
Mismatches 0; Indels 0;
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Matches 1041; Conservative
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1020 840 900 960 900 DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 7) human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG GGCAACAAGAGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG GGCAAAGTGGTAGATGGGCTGAATCAGGGCCTCCTTCGTGTACCTTATCGGGACAGCAAG CTCACTCGCCTATTGCAGGACTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGG Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate. protein" Disclosure, SEQ ID NO 7; 26pp; English. TCCAAGGAGGTGATCAATTGA 1041 Location/Qualifiers 1. .1464

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fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasis, treatenosis, cardiach hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 7) encoding a full length KID enzyme of the invention.
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                                                                                                               The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, and as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for
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GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG 900
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                                CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCCACAGTATCCTTATTGCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated microtubule motor protein, useful for screening modulat for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                              cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertroph; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthrigarit rejection; inflammatory bowel disease; angioplasty.
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                                                                                                                                                                                                                                                                                                                                                                                 Human microtubule motor protein DNA #4.
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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P-PSDB; ADQ60234.
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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "KID protein"
/transl_except= (pos: 1. .5; aa: Met)
/note= "This codon has an apparent 2 nucleotide insertion
that alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodilator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                  ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCGGG
         GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCTCGTGTACCTTATCGGGACAGCAAG
                                                  CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCACCCACAGTATCCTTATTGCCAAC
                                                                                    CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC
                                                                                                                                      ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCGGACTCAACTTTGCTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hyperriophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, procedures including surgery and proliferation induced after medical procedures including surgery and angioplasty, This sequence represents DNA encoding a human microtubule
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Pred. No. 3.4e-295;
0; Mismatches 1; Indels 0; (
                                                                                                                                                                                                Sequence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;
                                                                                                                                                       motor protein of the invention.
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Best Local Similarity 99.9
Matches 1039; Conservative
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therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 1) encoding a full length KID enzyme of the invention.
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                                                                                                                  Length 1115;
                                                                                  Sequence 1115 BP; 241 A; 318 C; 333 G; 223 T; 0 U; 0 Other;
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Pred. No. 3.9e-295;
0; Mismatches 0;
                                                                                                       99.7%; Scur-
100.0%; Pre
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Matches 1038; Conservative
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening cardial encoding them. The invention also relates to a method of screening for Appase activity of microtubule scimulated Arpase activity, a method of testing for Appase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target correction or act as a machilator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restences; cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restencist, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID on for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune conjugated after medical procedures including surgery and profile applace on order provention. Note: The specification states that this sequence encodes the protein featured as SEO ID NO:2, but this does not appear to be the case.
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978 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT
                                                                                       GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC
                                                                                                                                                       038 GCCCTGAGAGAGGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, microtubule motor protein, gene, ds, cellular proliferation disorder; cancer; hyperplasia, restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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2000US-00597292.
2000US-00724224.
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28-NOV-2000;
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1038 GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiliflammatoriies. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polymucleotide sequence is human KID DNA (SeqID 3) encoding a full length
                                                                                                                                                                                                                                                                                                                                                               1. .1538
/*tag= a
/produce = KID protein"
/produce = KID protein"
/transl except= (pos: 4. .5; aa: Pro)
/note= "This codon has an apparent 1 nucleotide deletion that alters the reading frame"
                                                                                                                                                                                                                ONA encoding the human kinesin-like DNA binding protein (KID) (SeqID 3)
                                                                                                                                                                                                                                            human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytosteatic; cardiant; immunomodulator; antiinflammatory; gene therapy; carder; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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20-JUN-2000;
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New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                 Human, microtubule motor protein, gene; ds; cellular proliferation disorder; cancer, hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angloplasty.
                                                                                                   Human microtubule motor protein
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
                                                                                                                                                                                                                             06-MAR-2002; 2002US-00093317
1098 AAGGAGGTGATCAATCG
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                       (CYTO-) CYTOKINETICS INC.
                                                                                                                                                                                                                                                                                                                          WPI; 2004-532491/51.
                                           ADQ60229 standard;
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                                                                              23-SEP-2004
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                                                               ADQ60229;
                                    ADQ60229
ID ADQ6
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for Arpase activity of microtubule atimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenoisis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenois, cardiac hypertrophy, immune disorders and inflammation, for treating disorders continent and for inhibiting KID and for treating disorders are used for associated with KID and for inhibiting KID and for treating cellular proliferation disorders and inflammation, for treating disorders continent associated with KID and for inhibiting KID and for treating autoimmune disorders and inflammation, for treating disorders continents associated with KID and for inhibiting KID and for treating autoimmune disorders are medical procedures including surgery and proliferation induced after medical procedures including surgery and construct protein of the invention. Note: The sequence resconders that this does not care protein of the protein featured as SEQ ID NO:4, but this does not appear to be the

Disclosure; SEQ ID NO 3; 26pp; English.

Score 1035.4; DB 12; Length 1538; Pred. No. 2.6e-294; 0; Mismatches 1; Indels 0; (Sequence 1538 BP; 355 A; 432 C; 459 G; 292 T; 0 U; 0 Other; . 0 99.5%; Query Match Best Local Similarity 99.9° Matches 1036; Conservative

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ADQ09241 standard; cDNA; 2097 BP

ADQ09241

(first entry)

23-SEP-2004

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The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of composition of modulating the expression of a gene responsive a THAP-foremoxine complex; (2) a pharmaceutical carrier; (3) a transcription factor decoy element in a pharmaceutical carrier; (3) a transcription factor decoy consisting assentially of a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy described above; (5) methods of consisting essentially of a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid encoding a THAP-family polypeptide; (8) a method of constructing a cell which expresses a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide; (9) methods of identifying a test compound that modulates transcription from sesociated with a condition mediated by a THAP/chemokine complex of a chemokine element or that modulated by a THAP/chemokine complex or insufficient apoptosis, cardiovascular disease and neurodegenerative associated with a condition selected from excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative or insufficient apoptosis, cardiovascular disease and neurodegenerative mediated by a THAP-family polypeptide in an individual; (1) a wector comprising a detectable product; (12) a genetically engineered cell acconding a detectable product; (12) a genetically engineered cell condition a that expression or condition to that expresses a THAP-family polypeptide in an individual; (12) a genetically by a that expression or that expresses a THAP-family polypeptide in an individual; (13) a condition and that expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
                                                                                                                                                                           thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator; human; gene; ss.
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                                                                                                                                   Human KNSL4 encoding cDNA SEQ ID NO:426
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ADK40995 standard; DNA; 2099

Novel human kinase gene #15.

(first entry)

06-MAY-2004 ADK40995;

ô polypeptide or its biological fragment; (13) an in vitro transcription reaction comprising a nucleic acid comprising a THAP responsive promoter, ribonucleotides and an RNA polymerase; and (14) an isolated mutant THAP-family polypeptide that does not bind to a chemokine. The pharmaceutical composition has antiangiogenic, antiinflammatory, cardiovascular, cytostatic, neuroprotective and osteopathic activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation us useful for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease or neurodegenerative present invention. 339 399 363 279 243 303 459 423 159 123 183 63 GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG 340 GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG GTGGCTGTGCGACTGCGCCATTTGTGGATGGAACAGCGGGGGCAAGTGATCCCCCCTGT GTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT GTGCGGGGCATGGACCAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT CTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTATGCA CTCAAATACCAGTTTGATGCCTTCTATGGGGAGGGAGTACTCAGCAGGACATCTATGCA GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC TATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG GTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCAAGGGAGGAGGGTGCCGAGGGC Gaps Query Match

99.5%; Score 1035.4; DB 12; Length 2097;

Best Local Similarity 99.9%; Pred. No. 3e-294;

Matches 1036; Conservative 0; Mismatches 1; Indels 0; Sequence 2097 BP; 483 A; 592 C; 628 G; 394 T; 0 U; 0 Other; 304 100 64 160 124 184 280 244 364 8ઠે 유 à g ò 셤 õ 셤 à g à a ò

The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and encodes a naturally occurring kinase polypeptide; (d) encodes the polypeptide in (a), except that it lacks one or more, but not all, of an N-terminal domain, C-terminal catalytic domain, a catalytic domain, a spacer region and a C-terminal domain, a coiled-coil structure region, a spacer region and a C-New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; pain; sexual dysfunction; mod disorder; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme; gene; ds. Claim 33; SEQ ID NO 102; 491pp; English. 31-DEC-2001; 2001US-0343169P 31-DEC-2002; 2002WO-US041687 ŝ Grigoriev IV, Sudarsanam (GRIG/) GRIGORIEV I V. (SUDA/) SUDARSANAM S. metabolic disorders. WPI; 2003-587115/55. WO2003057841-A2. Homo sapiens. ADK40995

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terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzhaimer's disease, viral infections infections caused by prions, infections caused by prions, infections caused by prions, infections caused by bacteria, infections caused by trions, infections caused by trions, infections caused by the sexual dysfunction, mood disorders, attention disorders, cognition disorders, dysfunction, mood disorders, attention disorders, neurological disorders, dysfunction, metabolic disorders and organ transplant rejection. This sequence corresponds to the DNA encoding one of the
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Best Local Similarity 99.9
Matches 1036; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
                     AACAAGGGCCTTCGGCTAAAAGAGAGTGGGGCCATCAACAACACCTCCCTGTTTGTCCTGGGC
                                                                                                                                                                                                                                               GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC
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99.3%; Score 1034; DB 3; Length 2104;
Best Local Similarity 99.7%; Pred. No. 7.7e-294;
Matches 1034; Conservative 1; Mismatches 2; Indels 0,
                                    Sequence 2104 BP; 517 A; 580 C; 597 G; 400 T; 0 U; 10 Other;
 s, wounds, and infectious represent sequences used
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for certain from a sequence acid sequences in forensics, in assessing biodiversities, or in identifying mutations cresponsible for genetic disorders and other traits. The nucleotide correspondences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide for generating antisense DNA or RNA. The present sequence for this patent did not form part of the printed specification, but was conclusion contains an expension of the printed specification, but was conclusion contains an expension of the printed specification, but was conclusion contains an expension of the printed specification, but was conclusions and directly from USPTO at
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GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCCAACTTTGCTGCCAGGTCC
                       1027 GCCCCTGAGAGAGACGCTTCTACCTAGACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC
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25.5%; Score 265; DB 9; Length 464;
Best Local Similarity 77.6%; Pred. No. 1.7e-67;
Matches 333; Conservative 0; Mismatches 95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                 Human; ss; sequencing by hybridisation; SBH; e.
genome mapping; biodiversity; genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stache-Crain
                                                                                                                                                                                                                BP
                                                                                                     1087 AAGGAGGTGATCAATCG 1103
                                                                                                                                                                                                                                                                                                                             Human foetal brain cDNA #5218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                  CDNA; 464
                                                                               1024 AAGGAGGTGATCAATTG
                                                                                                                                                                                                                                                                                           13-OCT-2003 (first entry)
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STACHE-CRAIN E
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRMANAC R T.
                                                                                                                                                                                                              ACH44493 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                       ACH44493;
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(STAC/) (DICK/) 1
(JONE/) 1
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ACH44493
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expression, comprising any of the 27,400 fully defined nucleotide
sequences in the specification, or their complements or fragments, and
cenceding at least 8 amino acids of any of the 6888 amino acid sequences
fully defined in the specification. The probe is a single exon probe that
cerversesed in human cells or tissues. Also included are a spatially-
addressable set of single exon nucleic acid probes for measuring human
cells or tissues. Also included are a spatially-
addressable set of single exon nucleic acid probes for measuring human
cent addressably isolatable or amplifiable from the plurality), a single
comparay for measuring human gene expression, a method of
measuring human gene expression, a vector comprising the single exon
cerver amino acids of any of the above-mentioned amino acid
contiguous amino acids of any of the above-mentioned amino acid
sequences (optionally with conservative amino acid substitutions), an
contiguous amino acids of any of the above-mentioned amino acid
sequences (optionally with conservative amino acid substitutions),
contiguous amino acids of any of the above mentioned of providing
contiguous amino acids of any of the above methods of selling and/or licensing single exon probes or microarrays to
a customer dealing to measure gene expression, a method of providing
chuman gene expression data by subscription, and a computer-readable
correct including data on the expression of a single exon probe
cited above. The probe, methods and apparatus are useful in gene
cypression analysis. The probes may be used as tools for surveying
clied above. The probes may be used as tools for surveying
clied above of an constructing genome-derived single exon microarrays.
Considered the presence of expressed messages that contain their
specific exon, or in constructing genome-derived single exon microarrays.

The probes are used in identifying and characterising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alternative splicing events, in detecting and characterising gross atterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744 GATTGACTTGGCTGGGTCAGAGACAACCGGCGCACAGGCCAACAAGGGCCTTCGGCTAAA 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 GATTGACTTGGCTGGGTCAGAGGACAACCGCCGCACAAGAGAGCCTTCGGCTAAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    804 AGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               864 TCAGGGCCTCCCTCGTGTATCCGGACAGCAAGCTCACTCGCCTATTGCAGGAC 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 ccaddridaccadcdaaacdriridaccccarrircaccagcgaagagaaaacrcraccr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 684 CAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCGAGAGGGAAAACTCTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 531 BP; 117 A; 153 C; 149 G; 112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 233.2; DB 12; Lenser
Pred. No. 4.2e-58;
3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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11 Similarity 98.7%;
235; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid probe for measuring human gene
                                                             CAAATACCAGTTTGATGCCTTCTATGGGGAGGAGTACTCAGCAGGACATCTATGCAGG
                                                                                                                                    217 CGTGCCTGAGGAGCTGGCATTAC-ATCTCGATGCTTGGCAGCCCAGAGCAACCTGGGGT
                                                                                                                                                                                                                                                                                                                                                      GCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAGA
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                                                                                                                                                                          TTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGTTGCCTA
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                                                                                                                                                                                                                                                                                                                                GATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGTGCCGAGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCCTGGACCCTGCGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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Length 531;

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20-MAY-2004
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                          g
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                                                                                 셤
                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide acquences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences concoling at least 8 amino acids of any of the 6888 amino acid sequences concoling at least 8 amino acids of any of the 6888 amino acid sequences concoling the propertion of the following the single exon prober is a single exon prober is a single exon prober of single exon nucleic acid probes for measuring human pare expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately concommitted and purality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately concommitted above, an ORF-encoded peptide comprising the single exon probes cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentioned any of the above-mentione any of the above-mentioned any acids and apparatus are useful in gene expression and above-mentions in the probes are used in identifying and characterising genome-detrived spanding and characterising any of a single exon microsoft or in expressing the ORF-encoded peptide of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             688 GTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCAGGAAAACTCTACCTGATT 747
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                                                                                                                                                                                                                                       New human genome-derived single exon nucleic acid probes useful for huma gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       748 GACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAG
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                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 24303; 80pp; English.
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                                                             03-APR-2002; 2002US-00029386.
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Best Local Similarity
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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      US2003194704-A1.
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                                  16-OCT-2003.
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R, Tamechika I;
867
                                                   AGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel human polynuclectide and the encoded polypeptide. A polynuclectide of the invention may have a use in gene therapy. An oligonuclectide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynuclectide or as a probe for detecting the polynuclectide. The polynuclectides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynuclectides are useful as pharmaceutical agents. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 TACCAGTITGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTATGCAGGTTCA
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                                                                                                                       GGCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGG
                                                                                                                                                    GCCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGG
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Pred. No. 1.6e-43;
0; Mismatches 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 249; 305pp; English
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Yoshikawa T,
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997 AAGCTCACCCGGCTCCTGAAGGACTCTCGGGAAACAGCCGCACAGGGATGATCGCT 1056
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406 CCCACAGGCTGTGGGAAAACCTACACCATGCTGGGCACAGACCAGGAGCCTGGCATCTAT 465
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Search completed: November 10, 2004, 06:57:56 Job time : 541.26 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	5,	7	Sequence 1, Appli	Sequence 3, Appli	Sequence 102, App	Sequence 288, App	Sequence 1180, Ap	Sequence 31705, A	Sequence 1177, Ap	Sequence 10603, A	Sequence 24303, A	Sequence 249, App
SUMMARIES	US-10-797-893-5	US-10-797-893-7	US-10-/97-893-1	US-10-797-893-3	US-10-334-143-102	US-09-925-300-288	US-10-087-192-1180	US-09-918-995-31705	US-10-087-192-1177	US-10-029-386-10603	US-10-029-386-24303	US-10-108-260A-249
DB	17	17	1	17	16	σ	13	10	13	15	15	16
% Query Match Length DB	1041	1464	5111	1538	2099	2104	24525	464	24291	531	232	2095
% Query Match	100.0	9.66	7.66	99.5	99.5	99.3	34.1	25.5	25.2	22.4	22.1	17.7
Score	1041	1038.4	1038	1035.4	1035.4	1034	355.4	265	262.4	233.2	230.4	184.6
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US-10-287-226-301 US-09-883-096-6 US-09-883-096-1 US-10-287-226-305	US-10-437-963-1460 US-10-152-319A-49B US-10-425-114-25129 US-10-425-115-148256 US-09-883-096-3	15551	10-336-472- 10-236-417- 10-172-118- 10-342-887- 10-302-172- 10-104-047-	US-10-159-563-34 US-10-369-493-27001 US-10-104-047-762 US-10-425-114-22135 US-10-739-930-2359 US-10-732-115-46568 US-10-172-118-1053 US-10-342-887-1053 US-10-424-599-111387 US-10-287-226-327 US-10-159-151-7
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ALIGNMENTS

61 AGGTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCC 120 61 AGGGTGGCTGTGCGACTGCGGCCATTTGTGGAACAGCGGGGGGGAGCAAGTGATCCCCCC 120 1 ATGGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTA 60 1 ATGGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTA Gaps ; 0 Length 1041; Sequence 5, Application US/10797893
; Sequence 5, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: 000411
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR PILING DATE: 2000-01-28
; PRIOR PILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FRSESO for Windows Version 4.0 0; Indels DB 17; Query Match
100.0%; Score 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1041; Conservative 0; Mismatches ORGANISM: Human LENGTH: 1041 US-10-797-893-5 SEQ ID NO 5 TYPE: DNA

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                                                                              GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCAGAATGCCAGTGTGTT
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                                      GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTT
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US-10-797-893-7
Sequence 7, Application US/10797893
Spublication No. US20040142397A1
GENERAL INFORMATION:
TITLE OF INVENTION: Obveil motor proteins and methods for TITLE OF. INVENTION: their use
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Pred. No. 0;
0; Mismatches
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
FRICK APPLICATION NUMBER: US/09/724,224
FRICK FILING DATE: 2000-11-28
FRICK APPLICATION NUMBER: 09/597,292
FRICK PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
SEQ ID NO 7
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Best Local Similarity 99.9
Matches 1039; Conservative
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; TYPE: DNA
; ORGANISM: Hume
US-10-797-893-7
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Qy 424 CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA 483 Db 498 CGGCCATGGGCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA 557 Qy 484 GACCTCCTGGACCCTGCTTCGGGAACCTGGTAATCCGAGAAGACTGCCGGGGAATATC 543 Db 558 GACCTCCTGGACCCTGCTTCGGGAACCTGGTAATCCGAGAAGACTGCCGGGGAATATC 617 Qy 544 CTGATTCCGGGTCTCCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC 603 Db 618 CTGATTCCGGGTCTCCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC 677 Qy 604 CTGCCAGCCACTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGGGCTCCTCCCGG 663 Db 678 CTGCCAGCCAGTGAAATCGGACTGTAGGAGCCACCAGGCTCAACCAGGGCTCCTCCCGG 737 Qy 664 AGTCATGCTGAAATCGGACTGTAGGAGCCACCAGGCTCAACCAGCGCTCCTCCCGG 737 Qy 664 AGTCATGCTGAAATCGGACTGTAGGAGCCACCAGGCTCAACCAGCGCTCCTCCCCGC 737 Qy 664 AGTCATGCTGAAATCGGACTGTAGGAGCCACCAGGCCTCCACCCCCCCTCCCCGC 737	Db 738 AGTCATGCTGTTCTTCTTCTTCTTCTTTTTTTTTTTTTT	RESULT 4 US-10-797-893-3 i Sequence 3, Application US/10797893 i Publication No. US20040142397A1 i GENERAL INFORMATION: i APPLICANTO No. US20040142397A1 i APPLICANTO No. UNABER USC i TITLE OF INVENTION: their use i TITLE OF INVENTION: their use i TITLE OF INVENTION: their use i TITLE OF INVENTION: their use i CURRENT APPLICATION NUMBER: US/09/724,224 i CURRENT FILING DATE: 2000-11-28 i PRIOR PILING DATE: 2000-11-28 i PRIOR APPLICATION NUMBER: US/09/724,224 i PRIOR PILING DATE: 2000-06-20 i WINDER OF SEQ ID NOS: 8 i SOFTWARE: FastSEQ for Windows Version 4.0 i SEQ ID NO 3 i LENGTH: 1538 i TYPE: DNA i ORGANISM: Human US-10-79-893-3 Query Match Best Local Similarity 99.9\$; Pred. No. 0; Matches 1036; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 781 GGCAACAAGGGCCTTCGGCTAAAAGAGGGGCATCAACACCTCCTGTTTGTCCTG 840 841 GGCAAAGTGGTAGTGGCATCGCTCCTGTTTGTCCTG 840 841 GGCAAAGTGGTAGTGGCTGATCGTTATCGGGACAGCAAG 900 841 GGCAAAGTGGTAGATGGGCTCCCTCGTGTACCTTATCGGGACAGCAAG 900 901 CTCACTCGCCTATTGCAGCACTCTGTGGGACAGCAAG 900 901 CTCACTCGCCTATTGCAGCACTCTGTGGGACACCAGTATTGCAAGAGACACTCTGTGTATCCTTATTGCCAAC 960 901 CTCACTCGCCTATTGCAGGACTCTCTGGGTGCTCAGCCAGTATCCTTATTGCTGCAAC 960 901 ATTGCCCTGAAGAGAGTGTCTCACTCAGCTCAGCACTCACT	RESULT 3 US-10-797-893-1 US-10-797-893-1 US-10-797-893-1 Sequence 1, Application US/10797893 Publication No. US2004014237A1 GENERAL INFORMATION: APPLICATUR: Beraud, Christophe TITLE OF INVENTION: World motor proteins and methods for TITLE OF INVENTION: Lot 4 TITLE OF INVENTION: Lot 4 TITLE OF INVENTION: WUMBER: US/10/797,893 CURRENT FILING DATE: 2000-10-28 PRIOR APPLICATION NUMBER: US/09/724,224 PRIOR PILING DATE: 2000-16-20 PRIOR PELING DATE: 2000-16-20 PRIOR FILING DATE: 2000-16-20 PRIOR FILING DATE: 2000-16-20 PRIOR FILING DATE: 2000-16-20 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 1115 TYPE: DNA TYPE: DNA TYPE: DNA GRANISM: Human US-10-797-893-1 Query Match Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;	0y 4 GGTCGCTGACCAAGCAACTAGAGCTACTCGTCCACCTCCAGCTCGCGTAAGG 63 18 11

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GGTCGCTGTCGCCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG
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RESULT 5

US-10-334-143-102

US-10-334-143-102

Sequence 102, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:

APPLICANT: GENGRIEV, IGOR VYACHESLAVOVICH

APPLICANT: GENGRIEV, IGOR VYACHESLAVOVICH

TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVE:

FILE REFERENCE: 036602/1543

CURRENT APPLICATION NUMBER: 105/10/334,143

CURRENT FILING DATE: 2002-12-31

PRIOR FILING DATE: 2001-12-31

PRIOR FILING DATE: 2001-12-31

SOFTWARE: PATCHIN UNC: 201

SOFTWARE: PATCHIN VOY: 2.1

SEQ ID NO 102.
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Best Local Similarity 99.9
Matches 1036; Conservative
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; ORGANISM: Homo sapiens
US-10-334-143-102
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
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| Sequence 288, Application US/09925300
| Patent No. US20020151681A1
| GENERAL INFORMATION:
| APPLICANT: Craig Rosen,
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PALO
| CURRENT APPLICATION NUMBER: US/09/925,300
| CURRENT PILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: F67/US00/05988
| PRIOR PILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1890
| SEQ ID NO 288
| LENGTH: 2104
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Pred. No. 0;
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
LOCATION: (44)
OTHER INPORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (497)
OTHER INPORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (1373)
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Best Local Similarity 99.7
Matches 1034; Conservative
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US-09-925-300-288
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Query Match
25.5%;
Best Local Similarity 77.6%;
Matches 333; Conservative 0
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                                               FEATURE:
NAME/KEY: misc_feature
                   ORGANISM: Homo sapiens
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US-09-918-995-31705
US-09-918-995-31705
Sequence 31705, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyeeq, Inc.
ITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
ITILE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REPEREENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31705
LENGTH: 464
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Pred. No. 2.3e-103;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PILING DATE: 2000-12-22
PRIOR PLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PEAGLEG for Windows Version 4.0
SEQ ID NO 1180
LENGTH: 24525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.8%;
Matches 445; Conservative
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; ORGANISM: Homo sapiens
US-10-087-192-1180
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                                                                                                                                   Score 265; DB 10; Length 464;
Pred. No. 1e-74;
0; Mismatches 95; Indels
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Publication No. US200201825861
GENERAL INFORMATION:
JAPPLICANT: Moris, David W.
APPLICANT: Engelhard, Eric K.
JITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ADVICER:
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT PAPLICATION NUMBER: US/09/747,377
PRIOR APPLICATION NUMBER: US/09/747,377
PRIOR APPLICATION NUMBER: US/09/798,586
PRIOR APPLICATION NUMBER: US/09/798,586
PRIOR FILING DATE: 2000-103-02
PRIOR APPLICATION NUMBER: US/09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE PEATSEQ FOR WINGOWS VERSION 4.0
; LOCATION: (1)...(464)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31705
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LOCATION: (1)...(24291)
OTHER INFORMATION: n = A,T,C or
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Sequence 24303, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA.X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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        CAAGGTGGACCAGGGGAACGTTTGGCCCCATTTCGCCAGCGAGAGGAAAACTCTACCT
                                        CCAGGTGGACCAGGGGGAAAACGTTTTGCCCATTTCGCCAGGGGAAAACTCTACCT
                                                                                                                    GATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCCAACAAGGGCCTTCGGCTAAA
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: WISSPROT HIT: 014807, EVALUE 5.00e-37

OTHER INFORMATION: ST HUMAN HIT: BE38282.1, EVALUE 1.00e-125

OTHER INFORMATION: NT HIT: 916453817, EVALUE 1.00e-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.6
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-029-386-24303
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US-10-108-260A-249
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                                                                                                                 2939 AGGTATTAGACCTCTTGGATCCTGCATCAGGAGACCTCGTGATCCGCGAAGACTGCCCAG 2998
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                                                                                    476 AGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGG
                                                                                                                                                                                            536 GGAATATCCTGATTCCCGGGTCTCCCCAGAAGCCCCATCAGTAGCTTTGCTGATTTTGAGC
                                                                                                                                                                                                                                                                                                           GGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCT
                                                                                                                                                                                                                                                                                                                                                               3059 AGCACTTCCTTCCAGCCAGTAGAAATCGAGCTGTAGGAGCCACCCGGCTTAACCAGCGCT
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                                  16;
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: NT HIT: AB017334.1, EVALUB 0.000+00

OTHER INFORMATION: SWISSPROT HIT: Q14807, EVALUB 2.000-36

OTHER INFORMATION: EST_HUMAN HIT: BF975048.1, EVALUE 1.000-126
     Pred. No. 2.2e-73;
0; Mismatches 61; Indels
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APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David R.
APPLICANT: Hankel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO TITLE OF INVENTION: EXPRESSION ANALYSIS TWO CURRENT APPLICATION NUMBER: US/10/029,386; CURRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION NUMBER: US/10/029,386; UNTRENT APPLICATION UNDER: US/10/029,386; UNTRENT US/10/03: 34288; UNTRENT US/10/03: 34288; UNTRENT US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: US/10/03: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER: UNDER:
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73.8%;
Best Local Similarity 73.8
Matches 385, Conservative
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Best Local Similarity 98.7
Matches 235; Conservative
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APPLICANT: Seringer, Olling A.M.,
APPLICANT: Zerhusen, Bryan D.,
APPLICANT: Zerhusen, Bryan D.,
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-4802
CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT PILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR PILING DATE: 2002-02-03
PRIOR PILING DATE: 2002-02-03
PRIOR PLING DATE: 2002-02-03
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR PLING DATE: 2002-08-13
PRIOR PLING DATE: 2002-08-13
PRIOR PLING DATE: 2002-08-13
PRIOR PLING DATE: 2002-08-14
PRIOR PLING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/384,409
PRIOR PLING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/384,409
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/334,627
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PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR PLING DATE: 2001-11-20
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NUMBER OF SEQ ID NOS: 673
SOFTWARE: CuraSeqList version 0.1
            Taupier, Jr., Raymond J., Vernet, Corine A.M.,
                                                                                                                                                                                           Sequence 301, Application US/10287226
Publication No. US20040086875A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Bdinger, Shlomit R.,
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Malyankar, Uriel M.,
MacDugall, John R.,
Mezes, Peter S.
Miller, Charles E.,
Miller, Isabelle,
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Spytek, Kimberley A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patturajan, Meera,
Rastelli, Luca.
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Ji, Weizhen,
Kekuda, Ramesh,
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Shenoy, Suresh G.
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Gangolli, Esha A.
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Ort, Tatiana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisen, Andrew,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 TGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAGACCTC 489
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                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 2095;
                                                                                                                                                                                                                                                                                                                                                                             Score 184.6; DB 16; Length
Pred. No. 1.3e-48;
0; Mismatches 379; Indels
TITLE OF INVENTION: No. US20040005560Alel full length cDNA FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTARRE: Patentin Ver. 2.1
SEQ ID NO 249
LENGTH: 2095
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.7%;
Matches 463; Conservative
                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-249
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                                                                                                              Length 3374;
                                                                                                             Score 155.8; DB 16; Length
Pred. No. 2.9e-39;
0; Mismatches 317; Indels
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ilarity 54.0%;
Conservative
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                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
                                                                       .. (3351)
                                                                                                            Query Match
Best Local Similarity
Matches 394; Conserv
                                                                         ; LOCATION: (7)
US-10-287-226-301
             LENGTH: 3374
SEQ ID NO 301
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                                                                                                               USE
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APPLICANT: Sakowicz, Roman
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
APPLICANT: Davies Katherine A.
ITILE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR FILE REPERBNCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 6
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ilarity 51.2%; Pred. No. 3.2e-33;
Conservative 0; Mismatches 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 6, Application US/09883096
Patent No. US20020110883A1
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew

RESULT 14 US-09-883-096-6

931 849

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ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCCACTCAACTTTGCTGCCAGG 1020
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JOTHER INFORMATION: Description of Artificial Sequence: HsKip3a gene. US-09-883-096-1.
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GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew
APPLICANT: Tu, Ming
APPLICANT: Tu, Ming
APPLICANT: Patel, Umesh A.
TITLE OF INVERTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 020552-001410US
CURRENT APPLICANT: 2001-06-15
FILE REFERENCE: 2000-06-15
FRIOR APPLICATION NUMBER: US 09/594,655
FRIOR APPLICATION NUMBER: US 09/594,655
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Patent No. US20020110883A1
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	nucleic - nucleic search, using sw model	Run on: November 9, 2004, 19:47:28; Search time 6796.66 Seconds (without alignments) 10701.074 Million cell updates/sec	Title: US-10-797-893-3 Perfect score: 1538 Sequence: 1 atgcagccgcggctcgaccattgtcccacaatgtga 1538	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 4526729 segs, 23644849745 residues	Total number of hits satisfying chosen parameters: 9053458	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1. ch ha.*	2: 9b_htg:* 3: 9b_ntg:* 4: qb_on:*	5: 9b_ov:* 6: 9b_pat:* 7: 9b_ph:*	8: gb_pl:* 9: gb_pr:* 10: gb_ro:*	11: gb_sts:* 12: gb_sy:* 13: gb_un:*	14: gb_vi:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution	SUMMARIES	Result Query No. Score Match Length DB ID Description	1538 100.0 1538 6 AR210053 AR210053	1530 99.5 1998 9 BT007259 1530 99.5 1998 12 BT007888 1530 99.5 2097 6 AR304057	1530 99.5 2097 9 1530 99.5 2117 9	1330 95.0 1134 9 DECOURSON 1461 95.0 1464 6 AR210055 1112.4 72.3 1115 6 AR210052	10 1074.8 69.9 2086 10 BC003427 11 1035.4 67.3 1041 6 AR210054 12 885.2 57.6 151041 2 AC101919	885.2 57.6 164759 10 AC101752 744 48.4 297639 2 AC101908 706.8 46.0 196674 10 AC102127	511.0 35.3 2750 5 ECUG3890 ECUG3890 510.2 33.2 2583 5 XLA249841 AJZ49841 508.6 33.1 2565 5 ECU43733 ECU43733 508.6 33.1 2640 5 ECU3177 ECU73177	

PRI 13-MAY-2003

Eisenstein, S., aer, J., Lin, Y.,

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Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
This CDS clone is a part of a collection of human full length
Eavyression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sall and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
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                                                                                                                   RVAVRLRPFVDGTAGASDPPCVRGMDSCSLEI ANWRNHQETILKYQFDAPYGERSTQQD
IYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTRE
EGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSF
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Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Direct Submission
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1998)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S. Kondinga,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y. Phelan,M. and Farmer,A.

Cloning of human full-length CDSs in BD Creator(TM) System Donor
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collection"
/lab_host="DH5alpha_T1 resistant"
/note="Vector: pDNR-Dual"
                                        TAGAGATTGAGAGGCTTAAGACGAAGCAAAAAAGAACTGGAGGCCAAGATGTTGGCCCAGA
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/codon_start=1
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/db_xref="taxon:9606"
/clone="GH00245X1.0"
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                                                                    CGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        CGGCGCACAGGCAACAAGGCCCTTCGGCTAAAAGAGAGGGGGGCCATCAACACCTCCCTG
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Tokai, N., Fujimoto-Nishiyama, A., Toyoshima, Y., Yonemura, S., Tsukita, S., Inoue, J. and Yamamota, T.
Kid, a novel kinesin-like DNA binding protein, is localized Chromosomes and the mitotic spindle
EMBO J. 15 (3), 457-467 (1996)
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Kid; kinesin-like DNA binding protein; kinesin family.
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R Beraud, C., Ohashi, C., Sakowicz, R., Vaisberg, E., Wood, K. and Yu, M. Human kinesins and methods of producing and purifying human kinesins

Rinesins

Rinesins

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1. 2097

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E 2 (bases 1 to 2097)
S Tokai-Nishizumi, N. and Edamasu, M.
Direct Submission
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D38751:Submitted (02-Nov-1994)
Sequence updated (25-Feb-1999).
Location/Qualifiers
1. 2097
Mol_type="MRNA"
Ab xrefe"Homo, sapiens"
//db xrefe"taxon:9606"
//close="MRNA"
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/cell_type="breast cancer"
1. .2097
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25. .2022
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I (bases 1 to 2117)

Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, M.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheeter, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzzy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Bone, S.J., and Marra, M.A., Schein, J.E., Jones, S.J., and Marra, M.A., Schein, J.E., Jones, S.J., Schent, J.E., Schein, J.E., Jones, S.J., Jone, J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co., J.Co.
                                                                                                                                                                     mRNA linear PRI 29-JUN-2004
22, mRNA (cDNA clone MGC:40049
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McCloskel,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at: http://image.llnl.gov Series: IRAK Plate: 62 Row: 1 Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-raip data
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1528 GAGGAAAAGGAGAACCATTGTCCCACAATG 1557
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                                                                                                                                                       Homo sapiens kinesin family member IMAGE:5241557), complete cds.
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                 ACCESSION
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IYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALLMDLLQLTRE
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ADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLA
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HGPPSQVEDLERVEGITGKQMESFLKANILGLAAGQRCGAS"
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GSAHSILIANIAPERRFYLDTVSALNPAARSKEVINRPFTNESLQPHALGPVKLSQKE
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                                                                                                        'clone="MGC:40049 IMAGE:5241557"
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99.5%; Score 1530; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                         note="Vector: pCMV-SPORT6"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Jordan, H., Morce, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casawant, T.L.,
Scheefz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Ioquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,
Villalon, D.K., Whuxny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Generation and mouse conA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: f Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andy Chae, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, Mr Santos, Angelique Schnerch, Ursula Skalska, Buane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
  PRI 29-JUN-2004
clone MGC:1573
                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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Contact: MGC help desk
Earll: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
2134 bp nily member 2
                         Homo sapiens kinesin family m
IMAGE:3535435), complete cds.
                                                                                                      BC004352.1 GI:13279307
                                                                                                                                                    Homo sapiens (human)
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     LOCUS
DEFINITION
                                                                                                                                                                           ORGANISM
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                            ACCESSION
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KEYWORDS
SOURCE
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COMMENT
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Beraud, C.
Motor proteins and methods for thei:
Motert: US 6387644-A 7 14 MAY-2002;
Location/Qualifiers

    1464
    /organism="unknown"
    /mol_type="unassigned DNA"

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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diacchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Uodin, T.B., Toshiyuki, S.,

Carnindi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Yillalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Ranchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myere, R.M.,

Butterfield, Y.S., Krzywinski, M. I., Skalska, U., Samailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Regeneration and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

BED 12477921
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21704181. Location/Qualifiers
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Submitted (20-FBB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
musculus kinesin family member 22, mRNA (cDNA clone MGC:6456
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                       MAGE:2615715), complete cds.
                                                                                                                  Mus musculus (house mouse)
Mus musculus
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BC003427.1 GI:13097359
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1. .2086 /gene="Kif22'

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ROD 29-JUN-2004

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      CAACCAGCGCTCCTCCCGCAGTCATGCTGTCCTGGTCAAGGTGGACCAGCGGGAACG
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db_xref="GI:13097360"
/note="synonym: Kid"
/db_xref="LocusID:110033"
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Mus musculus, clone RP24-158A6
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                                                                                                      DB 6; Length 1041;
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                                                                                                 Query Match 67.3%; Score 1035.4; DB 6
Best Local Similarity 99.9%; Pred. No. 4.9e-259;
Matches 1036; Conservative 0; Mismatches 1;
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                           65608 GAAGCGAAGGAGCACCCCTGTGTACGAGCCATAGACAGCTGCTCTTGAAGTGGCTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54770 TCATAGCATCCTCATTGTCAGCATTGCTCCTGAAAGATGTTTTTACCTGGATACAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGCAAGTGATCCCCCCTGTGTGCGGGCCATGGACAGCTGCTCTTAGAGATTGCTAAC
                                                                                                                                                               <u> ACTCAGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGG</u>
                                                                                                                                                                                                                                                                                                                           417 GGCAGCCCAGAGCAACCTGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                          AGGGAGGAGGGTGCCGAGGGCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAG
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                                                                                                                          Research
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                                                                                                                                    Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: 117745
Center project name: 117745
Center clone name: 1158_A 6
Center project name: 1187 A 6
Center project name: 1187 A 6
Center project name: 1187 A 6
Center project name: 1187 A 6
Center project name: 158 A 6
Center project name: 158 A 6
Center project name: 158 A 6
Center project name: 158 A 6
Consensus quality: 150558 bases at least Q40
Consensus quality: 150687 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 150741; suu-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 14, 2003 this sequence version replaced gi:28631351.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                   ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133517: contig of 33517 bp in length

1518 33617: gap of 100 bp

1618 42736: contig of 9119 bp in length

1737 42836: gap of 100 bp

1837 84394: contig of 41558 bp in length

1395 84494: gap of 100 bp

1495 151041: contig of 66547 bp in length.

Location/Qualifiers
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Pred. No. 1.1e-219;
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1. .33517
/note="assembly_fragment
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vector gide:left"
33618 42736
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/note="assembly_fragment"
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-158A6"
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vector_side:right"
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Best Local Similarity 78.2%;
Matches 1136; Conservative
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, Y., Chang, J., Chang, J., Choppel, Y., Collymore, A., Boukbgalter, B., Camarata, J., Chang, J., Choppel, Y., Collymore, A., Boukbgalter, B., Canarata, J., Chang, J., Choppel, Y., Collymore, A., Dodge, S., Dooley, K., Dorris, L., Bartis, B., Ball, M., Gage, D., Galagan, J., Gardyna, S., Rerreira, P., PitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Raratas, P., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., McZarthy, M., Meldrim, J., Meneus, L., Mihova, T., Misol, R., Norbu, C., O'Comnor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Renta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stange, Thondone, J., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Mguyen,C., Natcol,R., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramaeamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Spencer,B., Schauer,S., Schupbac,R., Seamen,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Wassiliev,H., Vonkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M..
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 164759)
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Center: Whitehead Institute/MIT Center for Genome Research
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/rpt_fam'
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                                                              -- CTAAGCAATATGGATCT 64489
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                                                                                                                                                                                                                                                                                     1373 GGCCCCTCTGTTGAGTACCCCAAAGCGAGAGGGGATGGTGCTAATGAAGACAGTAGAAGA 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                      1433 GAAGGACCTAGAGATTGAGAGGCTTAAGACGAAGCAAAAAGAACTGGAGGCCAAGATGTT 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC101752 164759 bp DNA linear ,ROD 23-APR-2004 Mus musculus chromosome 1, clone RP24-344C18, complete sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 164759)
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                                                                                                                                                                                                                                                                                                                                    1313 GGCCATGCTGGAGCGCCTCCTCAGCTTGGACCGTCTGCCTTGCCTCCCAGGGGAGCCAGGG
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                   64530 ATCTCCAGCATCTGCTTCCCAGAA----
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AC101752/c
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146080 CTGCTTCTAGCTGGAGTAAGGGTGGCTATATAATTGTGCCTGTTTGTGGGATGAAGAGACA 146021
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                                                                                                                                                                                                                                                                                                                                                                  297 ACTCAGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145242 TATACCATACCAGGAGGAGGCTCACTCGTTGTTGCAAGACTCTCTGAGAGGCTCAGC
                                                                                                                            GCGGCGGCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGT
                                                                                                                                                                                      CCACCTCCAGCTCGCGTAAGGGTGGCTGTGCGACTGCGGCCCATTTGTGGAATGGAACAGCG
                                                                                                                                                                                                                                                177 GGAGCAAGTGATCCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAAC
                                                                                                                                                                                                                                                                                                            TGGAGGAACCACCACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                 357 CAGAATGCCAGTGTGCTTGCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTG
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                                                             57.6%; Score 885.2; DB 10; Length 164759;
larity 78.2%; Pred. No. 1.1e-219;
Conservative 0; Mismatches 288; Indels 28; G
/rpt_family="(TA)n"
37958. .37986
/rpt_family="(GAA)n"
                                                              Query Match
Best Local Similarity
Matches 1136; Conserv
                      repeat_region
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Submitted (18-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 27, 2004 this sequence version replaced gi:31880232. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingron.edu/RM/RepeatWasker.html
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23 241322: gontig of 7622 bp in length
23 241322: gon of 100 bp
23 297659: contig of 56317 bp in length.
Location/Qualifiers
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="1"
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145182 TCATAGCATCGTTGTCAGCATTGCTCCTGAAAGATGTTTTTACCTGGAAACAATCTC 145123
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                      144900 AGCCATGTTGGGAAAGCTCCTGAGTATGATGTTTGCTGGGTTCCAAGGGGAGCCAGAG
                                                                        1073 CGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGAGAG
                                                                                                                                                                  145062 TGTACAACCTCAGGCCTTGACACCTGTTAAGCTGTCTCAGAAAGATCTGCTAGGTTTATC
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Mus musculus chromosome 1, clone RP24-275J1
Unpublished
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HTG; HTGS PHASE1; HTGS FUL
Mus musculus (house mouse)
Mus musculus
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musculus (house mouse)
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LOCUS
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                                                                                                                                                                                                                                                             GAAGCGAAGGAGCACCCCTGTGTACGAGCCATAGACAGCTGCTCTCTTGAAGTGGCTAAC 1029
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                                                                                                                                                                                                     CTGCTTCTAGCTGGAGTAAGGGTGGCTATATAATTGTGCCTGTTTGTGGATGAAGAGACA 1089
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                                                                                                                                                                          TGGAGGAAATACCAGGAGACTATCAAATATCAGTTTGATGCCTTCCATGGAGAAGAAGAGC 969
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                                                                                                                                                                                                                                                                                                                                                  ACTCAGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGG 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCAGCCCAGAGCAACCTGGGGTGATCCCGGGGCTCTCATGGACCTCCTGCAGCTCAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAGCCCAGAACAGCCTGGAAGTGATTCCTCAGACTCTCCCAGACCTCCTGCACTAACA 791
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                                                                                                                GCGGCGCCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGT
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                                                      Length 297639;
                                                                                   Indels
/clone="RP24-275J1"
/clone lib="RPCI-24 Male Mouse BAC"
                                                     Score 744; DB 2; I
Pred. No. 8.4e-183;
0; Mismatches 255;
                                                        48.4%;
llarity 78.0%;
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Matches 936;
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RESEARCH, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dases I to 196674)

Bi com, N. Nusbaun, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, Y., Bouslarkiy, L., Boukhgalter, P., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erreiras, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ferreiras, P., FitzGerald, M., Gage, D., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamar, A., Karates, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., McClean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCherthy, M., Meldrim, J., Manners, L., Minova, T., Minoya, T., Murphy, T., Noylor, J., Nguyen, C., Nguyen, T., Michang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., 1132 1193 AGAGGCAAAGAGCCGAGGCCCTGAGGAAGAGGAGTTGGGAGCCCTGAGGCCATGGC 1252 ROD 01-MAY-2004 131 250 TCATAGCATCCTCATTGTCAGCATTGCTCCTGAAAGATGTTTTTACCTGGATACAATCTC 191 71 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 196674) 1 AC102127 196674 bp DNA linear ROD 01-MAY-2 Mus musculus chromosome 1, clone RP23-202A19, complete sequence. AC102127 1073 CGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGAGAG 190 AGCATTAAACTTCACTGCTAGGTCCAAGGAGGTGATTAACCAGGCTTTCACCAAAGGGAG 130 TGTACAACCTCAGGCCTTGACACCTGTTAAGCTGTCTCAGAAAGATCTGCTAGGTTTAATC agagggaaagaaagccaaaagcccrcaagaagaarcaacrgggagcccrgagrcraragc Birren, B., Nusbaum, C. and Lander, B. Mus musculus chromosome 1, clone RP23-202A19 Unpublished

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repeat_region
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                          Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo.A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 196674)
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
Center project Information
Center project name: L18071
Center clone name: 202_A_19
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rpt_family="(CTA)n"</pre>
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(clone lib="RPCI-23 Female Mouse BAC"
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note="single clone coverage"
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/rpt_family="RLTRETN MM"
complement (1974. .2067)
/rpt_family="B4"
3219. .3319
/rpt_family="GA-rich"
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lone_end:SP6"_
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db_xref="taxon:10090"
'chromosome="1"
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JOURNAL
                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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/ppt fam.xy-
16809. 16866
/rpt family="(TG)n"
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rpt family="RMER20"
omplement(16008. .16517)
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/rpt_family="B4A"
complement (9243, .9815)
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omplement(5434..5561)
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509. .4638
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rpt_family="RSINE1"
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1230. .4235
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/rpt_family="(TG)n"
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785. .4832
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626. .3688
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833. .4955
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_family="Lx5"
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omplement(10373.
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196674; 12; Gaps	cccrgrgrgc ccrrgrgraa	GAGACTCTCA GAGAATACTA	TATGCAGGTT TAAGTAGGTT	CTTGCCTATG	GCAACCTGGG ACAACATGGA	TGCCGAGGGC TGCTGAAGGC	GAAGGTATTA AAAGGTATTA	GGGGAATATC	AGCGGCACTTC	SCTCCTCCGG	SATTICGCCAC	SGCGCACAGGC	TTGTCCTGGG(ACAGCAAGCTC	 acagaaaaat	FTGCCAACATI FTACCAACAC	CTGCCAGGTCC	CTGCTAGGTC	CCTTGGGACCT CTACACACCT	CCCGAGGCCC
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Score 706.8; DB 10; Pred. No. 4.2e-173; ; Mismatches 357;	143 TGTGCGACTGCGGCCATTTGTGGAACAGCGGGAGCAAGTGATCCCCCCTGTGTGCG	203 GGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACTCTCAA	ataccagtttgatgccttctatggggagagagtactcagcaggacatctatgcaggttc 	AGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGG	ACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGG	TGATCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGTGCCGAGGGCC	GGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCGGAGAAGGTATTAG 	ACCICCIGGACCCIGCTICGGAGACCIGGIAATCCGAGAAAAGACIGCCGGGGGAATATCC	TGATTCCGGGTCTCTCCCAGAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCC	TGCCAGCCAGTCGAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGCAATCGCAACCGGCTCTAACGAGAATCGGAATGAGAATAAAAAAAA	GTCATGCTGTGCTCCTGGTCAAGGTGGACCGGGGAACGTTTGGCCCCATTTCGCCAGGGGAACGTTTGGCCCCATTTCGCCAGGGGAACGTTTGGCCCCATTTTGCCAGGGTAACGTTTCAACTCTGTTTGAACTTTCAACTTAGATTTCAACTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTA	799 GAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCA 	ACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCA	ACCAGTGCATTCAACTCAAAGAGAGGCGCCATCAACACCTGCTTC-1101AC1GGGCA AAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCA		CTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATTG		zarrcrgagca	1099 AGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCTGCAGCCTCATGCCTTGGGACCTG	1159 TTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAGGCCCGAGGCCCTG 1218
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	Description	Adc23339 DNA encod	Adg60229 Human mic		Adk40995 Novel hum	Adc23343 DNA encod	Adg60233 Human mic	Aaf15853 Human pro	Adc23337 DNA encod	Adg60227 Human mic	Adc23341 DNA encod	Adq60231 Human mic	Abk70260 Human lun	Aas38879 Novel hum	Ach44493 Human foe	Ach77408 Human gen	Ach91108 Human gen	Adm01564 Human cDN	Ado44181 DNA encod	Adj95073 Novel NOV	Abx34596 Human mdd	Aba94614 Human kin
SUMMARIES	ΩI	ADC23339	ADQ60229	ADQ09241	ADK40995	ADC23343	ADQ60233	AAF15853	ADC23337	ADQ60227	ADC23341	ADQ60231	ABK70260	AAS38879	ACH44493	ACH77408	ACH91108	ADM01564	ADO44181	ADJ95073	ABX34596	ABA94614
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	22	138.6		4108	œ	ABS57215	Abs57215 Human kin
	23	137.2		2675	70	ADJ95077	Adj95077 Novel NOV
	24	136.6		1152	9	ABA94616	Aba94616 Nucleotid
	25	136.6		1152	8	ABS57216	Abs57216 DNA encod
	56	128.8		897	4	AAI70088	
	27	128.8	8.4	897	9	AAL39619	Aal39619 DNA encod
	28	128.8	w	897	12	ADM81051	Adm81051 Human HsK
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	31	126.6		1026	9	ABQ73061	Abg73061 Human kin
	32	126.6		1026	σ	AAL56806	Aal56806 DNA encod
	33	126.6		1026	10	ADB66785	Adb66785 DNA encod
	34	124.2		1011	9	ABQ73062	Abq73062 Human kin
	35	124.2		101	σ	AAL56807	Aal56807 DNA encod
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	37	121.8		3661	9	AAD28568	Aad28568 Human kin
	38	121.8		3694	10	ADC10189	Adc10189 Human NOV
	39	121.4		1014	9	ABA94615	Aba94615 Human H8K
	40	121.2		3570	12	ADQ19012	Adq19012 Human sof
	41	119.8		2994	4	ABL28591	Abl28591 Drosophil
	42	119.4		2034	4	ABL16733	Abl16733 Drosophil
	43	119.4		4034	4	ABL16732	Abl16732 Drosophil
	44	119.2		2132	10	ADC30338	Adc30338 Human nov
	45	117	7 7.6	1839	10	ADC30569	Adc30569 Human nov
						ALIGNMENTS	
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ADC	ADC23339						
a	ADC2	3339	ADC23339 standard; DNA;	; DNA;	1538	BP.	
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AC.	ADC2	ADC23339;					
X E	18-D	18-DEC-2003		(first entry)	<u> </u>		

fransl except= (pos: 4. .5; aa: Pro) /note= "This codon has an apparent 1 nucleotide deletion that alters the reading frame" DNA encoding the human kinesin-like DNA binding protein (KID) (SegID 3). human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. 1538
 *tag= a
 /product= "KID protein" Location/Qualifiers 28-NOV-2000; 2000US-00724224. 20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. (CYTO-) CYTOKINETICS INC. WPI; 2003-706919/67. P-PSDB; ADC23340. US6387644-B1. Homo sapiens 14-MAY-2002. Beraud C; Key

Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that

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DNA; 1538
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                                                                                                                                                                                           Sequence 1538 BP; 355 A; 432 C; 459 G; 292
                  Disclosure; SEQ ID NO 3; 26pp; English
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                                  ACCAGCGCTCCTCCCCCCAGTCATGCTGTGCTCCTGGTCAAGGTGAACGACCAGCGGGAACGTT
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Homo sapiens

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for medulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target compose, and included Arpase activity of a target protein, modulators of the target concein, and methods of treating cellular proliferation disorders such as another to protein, and methods of treating cellular proliferation disorders such as and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders and inflammation, for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune disorders and inflammation, for treating autoimmune consoluted with KID and for inhibiting KID and for treating autoimmune disorders and inflammation, for treating autoimmune consoluted with KID and for inhibiting KID and for treating autoimmune disorders and inflammation, for treating autoimmune consoluted after medical procedures including surgery and anglobatry. This sequence represents DNA encoding a human microtubule concodes the protein featured as SEQ ID NO:4, but this does not consolute the case.
                                                                                                                                                                                                                                                                                                                                                                                           New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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100.0%; Score 1538;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1538; Conservative 0; Mismatches
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                                                                                                                                                                               20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
                                                                                                                                   06-MAR-2002; 2002US-00093317
                                                                                                                                                                                                                                                                      (CYTO-) CYTOKINETICS INC
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                                              US6762043-B1
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TAGAGATTGAGAGGCTTAAGACGAAGCAAAAGAACTGGAGGCCAAGATGTTGGCCCAGA 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic acid.
                                                                                                                                                                                                                                        thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating expression of a Thanatos (death)-Associated Protein (THAP)
                                                                             1501 AGGCTGAGGAAAAGGAGAACCATTGTCCCACAATGTGA 1538
                                                                                            1501 AGGCTGAGGAAAAGGAGAACCATTGTCCCACAATGTGA 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clouaire
                                                                                                                                                                                                                       Human KNSL4 encoding cDNA SEQ ID NO:426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roussigne M,
                                                                                                                                                        ADQ09241 standard; cDNA; 2097 BP
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                          10-DEC-2002; 2002US-0432699P.
03-JUL-2003; 2003US-0485027P.
                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of of modulating the expression of a gene responsive to a THAP/fohenokine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a call comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a call comprising a viral vector which comprises a promoter operably linked fragment; (7) a method of constructing a cell which expresses a fragment; (7) a method of constructing a cell which expresses a combinant THAP-family polypeptide or its biological fragment; (8) a method of ameliorating symptoms associated with a condition mediated by a THAP/chemokine complex Example 47; SEQ ID NO 426; 612pp; English.

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at a THAP responsive element or that modulates the transport of a chemokine into the nucleus; (10) methods for reducing the symptoms associated with a condition selected from excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative diseases; symptoms associated with a condition resulting from the activity of a chemokine or a THAP-family polypeptide in an individual; or symptoms associated with transcriptional repression or activation comprising a THAP-family polypeptide in an individual; (11) a vector comprising the vector described above or that expresses a THAP-family polypeptide in an individual; (12) a vector comprising the vector described above or that expresses a THAP-family polypeptide or its biological fragment; (13) an in vitro transcription reaction comprising a nucleic acid comprising a THAP responsive promoter; (13) an in vitro transcription reaction comprising an antaleic acid comprising a THAP responsive promoter; (13) an in vitro transcription cannocitic that does not bind to a chemokine. The pharmaceutical composition has antiangiogenic, antiinflammatory, cardiovascular, composition has antiangiogenic, antiinflammatory, cardiovascular, composition has antiangiogenic, antiinflammatory, cardiovascular, composition has antiangiogenic, antiinflammatory, cardiovascular, composition the expression of a THAP responsive gene. Modulation us useful confinent and antiqued and an expensive or insufficient and enginesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient and enginesis, inflammation, metastasis of a cancerous expenses; inflammation, metastasis of a cancerous expenses; inflammation, metastasis of a cancerous expenses; inflammation, metastasis of a cancerous expenses; inflammation, metastasis of a cancerous expenses; inflammation, metastasis of a cancerous expenses; in the expression of a THAP exponsive promoterial vector and promoterial vector and promoterial
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antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; occular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme; gene; ds.

31-DEC-2002; 2002WO-US041687 31-DEC-2001; 2001US-0343169P

WO2003057841-A2. Homo sapiens.

17-JUL-2003

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Grigoriev IV, Sudarsanam

WPI; 2003-587115/55.

(GRIG/) GRIGORIEV I V. (SUDA/) SUDARSANAM S.

noot ropic;

neuroprotective;

cytostatic; immunomodulator; cardiant;

human kinase gene #15.

Novel

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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and conditions to (a) and conditions to (a) and conditions to (b) and conditions to (a) and conditions of a condition of a condition of an except that it lacks one or more, but not all, of an N-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, pair, viral infections infections caused by fund; ocular diseases, methodic anseed by fund; ocular diseases, methodic anseed by fund; ocular diseases, methodic anseed by fund; ocular diseases, methodic alsorders, disorders, effection, This sequence corresponds to the DNA encoding one of the
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kinase polypeptide, useful for treating cancer, immune-related diseases,
cardiovascular disease, brain or neuronal-associated diseases and
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1468 1288 1385 1408 1444 1504 This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 7) human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. AGTACCCCAAAGCGAGGCGGATGGTGCTAATGAAGACAGTAGAAGAGAAGACCTAG-A GATTGAGAGGCTTAAGACGAAGCAAAAAGAACTGGAGGCCAAGATGTTGGCCCCAGAAGGC GCCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAG CGCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGGAGCCAGGGGGCCCCTCTGTTG Identifying a candidate agent as modulator of function of a targ protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate. TGAGGAAAAGGAGAACCATTGTCCCACAATG 1535 "KID protein" Disclosure; SEQ ID NO 7; 26pp; English

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domains, such that the target protein directly or indirectly produces ADP cor phosphate. Furthermore, this activity of an be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a finesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunoamodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, trestenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleoride sequence is human KID DNA (SeqID 7) encoding a full length KID enzyme of the invention.
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                                                                                                                                              95.0%; Score 1461; DB 10; Length 1464; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels 0;
                                                                                                                           Sequence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or completed or activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders as and inflammation, for treating disorders associated with kinesin-like DNA creening for modulators of motor proteins useful for treating cellular complication disorders and as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune completed with KID and for inhibiting KID and for treating autoimmune disorders and inflammation, for treating autoimmune disease, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasisy. This sequence represents DNA encoding a human microtubule completed in the invention.
                                                                                                                                                                                                                                                                                       New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 7; 26pp; English.
                                           20-APR-1999; 99US-00295612
20-JUN-2000; 2000US-00597292
28-NOV-2000; 2000US-00724224
06-MAR-2002; 2002US-00093317
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95.0%; Score 1461; DB 12; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                          Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rare cancer associated gene sequences, referred to as prostate cancer aens, useful for treatment, prevention, and diagnosis of disorders as prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPISSES to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, undonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 805-806; 2338pp; English.
                                                       AAF15853 standard; cDNA; 2104 BP
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(ROSE/) ROSEN C A.
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method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 1) encoding a full length KID enzyme of the invention.
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                                                                                                                                                         Sequence 1115 BP; 241 A; 318 C; 333 G; 223 T; 0 U; 0 Other;
                                                                                                                                                                                             Score 1112.4; DB 10; Lengt
Pred. No. 6.5e-296;
0; Mismatches 1; Indels
                                                                                                                                                                                           Query Match 72.3%;
Best Local Similarity 99.9%;
Matches 1113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA binding protein (KID) (SeqID 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                             CCINCAGCTIGGACCGTCTGCTTGCCTCCCAGGGGAGCCAACGGGGCCCCTCTGTTGAGTA
                                                                                                                         AGAGGCTTAAGACGAAGCAAAAAGAACTGGAGGCCAAGATGTTGGCCCAGAAGGCTGAGG
                                                                                                                                                                                                 CCCCAAAGCGAGGCGGATGGTGCTAATGAAGACAGTAGAAGAAGAAGCACCTAGAGATTG
                       CCT-CAGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGCCCCTCTGTTGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide
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P-PSDB; ADC23338.
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                                                                                         Sequence 1115 BP; 241 A; 318
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein or act as a modulator of the binding characteristics or concer, hyperplasias, restenosis, cardiac hypertrephy, immune disorders and inflammation, for treating cellular proliferation disorders as and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
       ATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA
                                                     ATCGGGACAGCAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA
                                                                                                                                                                                                                                                                                                                      Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                1114
                                                                                                                                                         ACTITIGCTGCCAGGTCCAAGGAGGTGATCAATTG 1114
                                                                                                                                               ACTITIGCTGCCAGGTCCAAGGAGGTGATCG
                                                                                                                                                                                                                                                                                                 Human microtubule motor protein DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1; 26pp; English.
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubules motor protein of the invention. Note: The specification states that this sequence encodes the protein featured as SEQ ID NO:2, but this does not
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therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 5) encoding a full length KID enzyme of the invention.
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Pred. No. 1.1e-274;
0; Mismatches 1; Indels 0;
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Best Local Similarity 99.9%;
Matches 1036; Conservative (
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                                     the human kinesin-like DNA binding protein (KID) (SeqID
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904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                   cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kineain-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                       GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                          "Human microtubule motor protein #3"
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                                                                                    AAGGAGGTGATCAATTG 1040
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2000US-00597292.
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diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubule
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                                                                                                                                                                                         Score 1035.4; DB 12;
Pred. No. 1.1e-274;
); Mismatches 1; I
                                                                                                                                      Sequence 1041 BP; 228 A; 295 C; 302
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                                                                                     motor protein of the invention.
                                                                                                                                                                                         Query Match 67.3%;
Best Local Similarity 99.9%;
Matches 1036; Conservative
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RESULT 13
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or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the collynucleotide operably linked to an expression vector of; an isolated collynucleotide operably linked to an expression vector of; an isolated collynucleotide operably linked to an expression vector of; an isolated or transfected with an expression vector of; an isolated or altipoptide; a method for detecting the presence of a cancer in a patient of a fusion protein comprising at least the polypeptide; an oblypeptide; an exthod for etiminating and/or expanding T cells of specific for tumour protein; an isolated T cell population comprising T colls specific for tumour protein; an isolated T cell population comprising a first component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second proteins. T cell populations and antigen presenting cells expressing the polymorleotides, proteins, and a patient by administering the composition and diagnostic kits comprising at least one of the oligonucleotide of, or an antibody and a contract in a patient by administering the presenting to proper presenting of a reporter group. The polypeptides, and a reporter group. The polypeptides, and a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group. The polypeptides of a reporter group of a reporter group of a reporter group.
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904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tumor lung proteins and nucleic acids encoding the proteins, useful as vaccines and for treating, preventing, diagnosing or monitoring lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 88; gene; lung cancer; cytostatic; tumour; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer associated cDNA SEQ ID 131
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                                                                                                                                                                                                                         AAGGAGGTGATCAATTG 1040
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                                                                                                                                                                                   1098 AAGGAGGTGATCAATCG 1114
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10-OCT-2000; 2000US-0239440P.
29-JUN-2001; 2001US-0301928P.
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                                                                                                                                                                                                                                                                                                                                                CTCCGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGA
                                                                                                                                                                                                                                                                                                                                                                               61 CTCCGCACTCTAGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTT-CCAATGA
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inhibiting expression of tumour polypeptides and proteins in tumour cells. The present sequence is one of the 183 lung cancer associated polynucleotides
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                 1;
                                                                                                                                                 Length 491;
                                                                                                C; 136 G; 88 T; 0 U; 0 Other;
                                                                                                                                                                                            0; Indels
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                                                                                                                                            Score 480; DB 6; L
Pred. No. 9.3e-122;
0; Mismatches 0;
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                                                                                                                                            31.2%;
99.8%;
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                                                                                                Sequence 491 BP; 127 A; 140
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                                                                                                                                                                        Best Local Similarity 99.8
Matches 491; Conservative
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                                                                                                                                                                                                                           The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding
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genome mapping; biodiversity; genetic disorder.
                                                                                                                                treatment
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        Lamson
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                                                                                                                           New polynucleotides and polypeptides, useful for diagnosis and of breast, lung and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 376.4; DB 4; Length 386; Pred. No. 3e-93;
                          Drmanac S, Labat I; WL, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 386 BP; 105 A; 102 C; 118 G; 61 T; 0 U; 0 Other;
        Кавваш А,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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      Pot D,
                                           Jones WL,
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    Randazzo F, Kennedy GC,
Crkvenjakov R, Dickson M,
), Kita D, Garcia V, Jone
                                                                                                                                                                                        Claim 1; Page 1080; 1193pp; English
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ilarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       sequences of the invention
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                                                                                    WPI; 2001-530177/58
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Best Local Similarity
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Reinhard C,
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Matches 380;
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/RST sequences. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA libraries, useful
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30-JUL-2001; 2001US-00918995.
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JONES L W.
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96

216 439 275 499 335 559

smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at

Sequence 531 BP; 117 A; 153 C; 149 G; 112 T; 0 U; 0 Other;

segdata.uspto.gov/sequence.html?DocID=20030194704

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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
396 CCTCCTGGACCCTGCTTCGGGAGACCTTGGAATCCGAGAAGACTGCCGGGGGAATATCCT 455
                                                                                                                                                 Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                              Human genome derived single exon probe #10603.
                                                                                                                                                                                                                                                                                                                                                                             Claim 15; SEQ ID NO 10603; 80pp; English.
                                                                            ACH77408 standard; DNA; 531 BP.
                                                                                                                                                                                                                                                                                                 Penn SG, Rank DR, Hanzel DK
                                                                                                                                                                                                                             03-APR-2002; 2002US-00029386.
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                                  GATTCCGGG 464
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide captression, comprising any of the 27,400 fully defined nucleotide expression, acids of any of the 6888 amino acid sequences conciding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that controlled acid sequences controlled in the specification. The probe is a single exon probe that the specification. The probe is a single expressed in human cells or tissues. Also included are a spatially-captressed in human cells or tissues. Also included are a spatially-captressed in human cells or amplifiable from the plurality), a single controlled advove, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a wector comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acids of any of the above-mentioned amino acids of selling and/or licensing single exon probes or microarrays to solated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to contage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods may be used as tools for surveying cited above. The probe, methods may be used as tools for surveying cited above. The probes may be used as tools for surveying cited above. The probes may be used as tools for surveying cited above. The probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising specific.

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100.0%; Pred. No. 0;
ive 0; Mismatches
SQUENCE 3. Application US/09724224
Facent No. 6387644
GENERAL INFORMATION:
APPLICANT: BERAUGH Christophe
TITLE OF INVENTION: No. 6387644e1 motor prote
TITLE OF INVENTION: US. 6387644e1 motor prote
TITLE OF INVENTION: US. 09/724,224
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 3
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US-10-03-317-3
(Sequence 3, Application US/10093317
; Patent No. 6762043
; Patent No. 6762043
; GENREAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; RAIOR APPLICATION NUMBER: 09/724,224
; RAIOR PAPLICATION NUMBER: 09/724,224
; RAIOR PAPLICATION NUMBER: 09/724,224
; RAIOR PAPLICATION NUMBER: 09/724,224
; RAIOR APPLICATION NUMBER: 09/724,224
; RAIOR APPLICATION NUMBER: 09/724,224
; RAIOR PILING DATE: 2000-11-28
; SOFTWARE: FASTESQ for Windows Version 4.0
; SEQ ID NO 3
LENGTH: 1538
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100.0%; Score 1538;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1538; Conservative 0; Mismatches
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US-10-093-317-3
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APPLICANT: Yu, Ming
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: Human kinesins
FILE REFERENCE: CYCOPO36
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                              TYPE: DNA
ORGANISM: Human
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Sequence 34, Application US/09595684B
Patent No. 6544766
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: Vaisberg, Eugeni

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; Sequence 7, Application US/09724224
; Patchet No. 6387644
; GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor prot-
TITLE OF INVENTION: their use
FILE REPERENCE: 104
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-620
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
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Matches 1461; Conservative
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95.0%; Score 1461; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches
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; ORGANISM: Human
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Patent No. 6762043

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6762043el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/10/093,317

CURRENT FILING DATE: 2002-03-06

PRIOR APPLICATION NUMBER: 09/724,224

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 8
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor proteins and methods for
TITLE OF INVENTION: No. 6387644el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 104
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT APPLICATION NUMBER: 09/597,292
PRIOR PILING DATE: 2000-16-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1115
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Pred. No. 3.1e-309;
0; Mismatches 1;
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US-09-724-224-1
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; Patent No. 6387644
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Best Local Similarity 99.9
Matches 1113; Conservative
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ORGANISM: Human
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US-09-724-224-1
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RESULT 8 US-09-724-224-5

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; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT APPLICATION NUMBER: 09/597,292
; PRIOR RILING DATE: 2000-06-20
; NUMBER OF SEC ID NOS: 8
; SCOTUMARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Human
US-09-724-224-5 Length 1041; ö for Indels Score 1035.4; DB 3; Pred. No. 3.8e-287; 0; Mismatches 1; I Query Match 67.3%; Best Local Similarity 99.9%; Matches 1036; Conservative 798 8

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APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Patel, Umesh A.
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/10093317; Patent No. 6762043; CENERAL INFORMATION: APPLICANT: Beraud, Christophe; TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use; FILE REFERENCE: 1044; CURRENT FILING DATE: 2002-03-06; PRIOR APPLICATION NUMBER: US/10/093,317; CURRENT FILING DATE: 2000-11-28; NUMBER OF SEQ ID NOS: 8; SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Human
US-10-093-317-5
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APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew
APPLICANT: Craven, Andrew
APPLICANT: Craven, Andrew
APPLICANT: Sakowicz, Roman
APPLICANT: Patel, Umesh A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
SOFWRARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
SENERAL INFORMATION:
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                                                                                      Gaps
OTHER INFORMATION: protein gene HeKip3a (Figure 1).
OTHER INFORMATION: Description of Artificial Sequence: HsKip3a gene
                                                                                   27;
                                                        DB 4; Length 4108;
                                                     Query Match 9.0%; Score 138.6; DB 4; Length Best Local Similarity 51.0%; Pred. No. 1.8e-29; Matches 448; Conservative 0; Mismatches 404; Indels
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: HsKip3a OTHER INFORMATION: fragment OTHER INFORMATION: Nucleotide sequence of HsKip3a fragment used OTHER INFORMATION: ATPage asgay (Figure 5).
                                                                                                                                                                                                               27;
                                                                                                                                                                                                               Indels
                                                                                                                                                                  Score 136.6; DB 4;
Pred. No. 3.5e-29;
0; Mismatches 389;
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Best Local Similarity 51.2%;
Matches 437; Conservative (
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RESULT 11 18-09-883-096-6 ; Sequence 6, Application US/09883096 ; Patent No. 6680369

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384 CCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGTGATC 443
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; LOCATION: (4772)...(495)
; OTHER INFORMATION: n = a, C, t,
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Matches 430; Conservative
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ORGANISM: Human
FEATURE:
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                                                                                                             CCCACAGGCTGTGGGGAAAACCTACACCATGCTGGGCACAGACCAGGAGCCTGGCATCTAT 285
                                   Crcaardecrridecegardeaaaggecedeaagaececardrecerracedegaedeaaa 921
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; Batent No. 6294371
; GBNERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Breedman, Richard
; TITLE OF INVENTION: No. 6294371el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1045
; CURRENT APPLICATION NUMBER: 0200-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO :
LENGTH: 897
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8.4%; Score 128.8; DB 3; Length 897;
Best Local Similarity 50.1%; Pred. No. 5.4e-27;
Matches 430; Conservative 0; Mismatches 356; Indels 72
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ORGANISM: Human
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; Sequence 1, Application US/09724508
; Patent No. 6368841
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6368841el motor proteins and methods for
; TITLE OF INVENTION: their use
; TILE REFERENCE: 1045
; CURRENT APPLICATION NUMBER: US/09/724,508
; CURRENT FILING DATE: 2000-11-27
; PRIOR PAPLICATION NUMBER: 09/621,233
; PRIOR PILING DATE: 2000-07-21
; SOFTWARE: PRESENCE for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 897
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Pred. No. 5.4e-27;
0; Mismatches 356; Indels 72
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Pactent No. 6391573

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: No. 6391573el motor proteins and methods for TITLE OF INVENTION: their use

FILE REFERENCE: 1045

CURRENT FILING DATE: 2000-11-27

PRIOR PAPLICATION NUMBER: 09/621,233

PRIOR FILING DATE: 2000-12-27

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PRESENCE for Windows Version 4.0

SEQ ID NO 1

LENGTH: 997
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ORGANISM: Human
PEATURE:
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Pred. No. 5.4e-27;
0; Mismatches 356;
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US-10-090-695-1
; Sequence 1, Application US/10090695
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Best Local Similarity 50.1'
Matches 430; Conservative
; NAME/KEY: misc_feature
; LOCATION: (472)...(495)
; OTHER INFORMATION: n = a,
US-09-724-516-1
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APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 664072el motor proteins and methods for
TITLE OF INVENTION: No. 664072el motor proteins and methods for
TITLE OF INVENTION: Heir use
CURRENT FILING NATION NUMBER: US/10/090,695
CURRENT FILING DATE: 2002-03-04
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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8.4%; Score 128.8; DB 4; Length 897;
Best Local Similarity 50.1%; Pred. No. 5.4e-27;
Matches 430; Conservative 0; Mismatches 356; Indels 72.
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
i LOCATION: (472)...(495)
i OTHER INFORMATION: n = a, c, t, or g
US-10-090-695-1
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 897
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November 10, 2004, 13:18:18; Search time 820.883 Seconds (without alignments) 10087.639 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/Pcr_NEW PUB.seq:*
2: /cgn2 6/ptodata/1/pubpna/Pcr_NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/Pcr_NEW PUB.seq:*
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5: /cgn2 6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
6: /cgn2 6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
7: /cgn2 6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
8: /cgn2 6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
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16: /cgn2 6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2 6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
18: /cgn2 6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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10: /cgn2 6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1538
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli Sequence 102, Appli Sequence 288, Appli Sequence 1, Appli Sequence 1, Appli Sequence 131, Appli Sequence 131, Appli Sequence 1180, Appli Sequence 1180, Appli Sequence 1180, Appli Sequence 11705, Appli Sequence 11705, Appli Sequence 11705, Appli	
SUMMARIES	US-10-797-893-3 US-10-334-143-102 US-10-334-143-102 US-10-797-893-7 US-10-797-893-1 US-10-797-893-5 US-09-960-253-131 US-09-803-719-1937 US-10-087-192-1180 US-10-087-192-1180 US-10-087-192-1177 US-10-087-192-1177 US-10-087-192-1177	
DB	17 17 17 17 17 17 17 17 17 17 17 17	
* Query Match Length DB ID	24 464 464 464 464 464 464 464 464 464 4	
% Query Match	100.0 98.0 95.0 94.3 72.3 31.2 24.5 24.5 17.1 15.2	
Score	1538 1519 1519 1450.2 1112.4 1015.4 376.4 376.4 265.4 233.2	
Result No.	11000011111111111111111111111111111111	

Sequence 24303, A Sequence 249, App Sequence 10, Applications of Applications	105
US-10-029-386-24103 US-10-108-260A-249 US-10-108-260A-249 US-10-287-226-301 US-09-883-096-6 US-10-287-226-305 US-09-883-096-6 US-10-437-963-1460 US-10-437-963-1460 US-10-425-115-148256 US-10-425-115-148256 US-10-425-115-148256 US-10-311-642-3 US-10-311-642-3 US-10-31-642-3 US-10-31-542-8 US-10-076-555-324 US-10-076-555-324 US-10-076-555-334 US-10-36-37-263-555-384 US-10-36-37-263-555-384 US-10-36-38-472-23 US-10-36-38-472-23 US-10-36-38-472-23 US-10-36-38-472-23 US-10-36-38-472-38 US-10-172-118-1087 US-10-172-118-1087 US-10-172-114-22135 US-10-172-114-22135 US-10-133-930-2359 US-10-133-937-34 US-10-133-937-37-34 US-10-133-93-277011 US-10-133-93-277011 US-10-133-93-277011 US-10-133-93-277011	US-10-172-118-1053
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ALIGNMENTS

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Sequence 3. Application US/10797893
; Sequence 3. Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/99/724,224
; PRIOR APPLICATION NUMBER: US/99/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NOS: 8
; SEQ ID NOS: 8
; FANTALL APPLICATION NUMBER: US/997,292
; NUMBER OF SEQ ID NOS: 8
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Best Local Similarity 100.
Matches 1538; Conservative
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9 9 CGGCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCAC 120 CGGCGATCTCAGGAGCTGGTCGCTGTCGCTAAGCAAGATTGGAGCTACTCGTCGTCCAC 120

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g 8

	102 No. US20040009549A1 No. US20040009549A1 RMATION: GRIGORIEV, IGOR VYACHESLAVOVICH GRIGORIEV, IGOR VYACHESLAVOVICH GRIGORIEV, IGOR VYACHESLAVOVICH GRIGORIEV, IGOR VYACHESLAVOVICH SUDARSANAM, SUCHA VENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES VENTION: KINASES IDENTIFIED WITH THE METHOD LICATION NUMBER: US/10/334,143 LICATION NUMBER: 60/343,169 G DATE: 2001-12-31 EQ ID NOS: 207 atentin Ver. 2.1 99 Homo sapiens	Query Match 98.8%; Score 1519; DB 16; Length 2099; Best Local Similarity 99.9%; Pred. No. 0; Matches 1530; Conservative 0; Mismatches 0; Indels 1; Gaps 1; Qy 6 GCCGCGGGCCCCACACGCACACGCACACGCACACCCACC
CTCCAGCTCGCGTAAGGGTGGCTGTGCGGCCATTTGTGGATGGA	AGGAGGTGCCGAGGGCCGGCCATTGCTGTCACCATGTCTTACCTAGGATCT AGGAGGGTGCCGAGGGCCGTGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCT ACCAGGAGAGGTGCCGGCCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCT ACCAGGAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAG ACTGCCGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGGCCTGTGTAATCCGGAAG ACTGCCGGGGGAATATCCTGATTCCGGGTCTCTCCCCAGAAGCCCATGAGATATCCTGATTTGTGCTGATTTTGAGCGGGAATATCCTGCTGTTTCCCCAGAAGCCCATCAGTAGCTTTTGTGTGAATTTTGAGCGGGAATATCCTGCTGTTTTGAGCGGGAATATCCTGCTGTTTTTGAGCGGGAATATCCTGCTGTTTTGAGCGGGAATTTTGAGCGGCACTTCCTGCTGTTTTGAGCGGCACTTCCTGCCAGTCGTTTTGTTTTGAGCGGCACTTCCTGCCAGTCGTTTTGTTTTGAGCGGCACTTCCTGCTGAATTCGAAATCGGAACTCTTTGAGCGGCACCCCGGGCTCATTTTGAGCGGCACTCCTGGCCAGTCGTAGGACCCCCGGGCTCATTTTGAGCGGCACTCCTGGCTCAAGGTCGGGAACGTTTACCCCGGGGAACGTTTACCCCGCGGGAACGTTTACCCCGGGGAACGTTTAACCTTCGCCAGTCGAAGGTCGAAGGTCGGGAACGTTTAACCTTCGCCAGTTTAACCTTGGCTCGAAGGTCGAACGTTTTAACCTTCGCCAATTGACTTGGCTCGAAGGTTGAACGTTTTAACCTTCGCCAATTGACTTGACTTGGCTCGAAGGTTGAACTTTGACTCGAAGGTTGAACGTTTTAACCTTAACTTTGACCGAAACCTTTTTAACCCCCAATTCGCTCGAACGTTTTTAACCTTAACACTTTAACCTTAACACTTTTAACCTTAACACTTTTAACCTTAACACTTTTAACCTTAACACTTTAACTTTTAACCTTAACACTTTAACTTTAACCTTAACACTTTTAACCTTAACACTTTAACTTTAACCTTAACACTTTTTT	181 TGGCCCATTTGGCCAGGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGG 840

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CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC 677
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1445 GATTGAGAGGCTTAAGACGAAGCAAAAGAACTGGAGGCCAAGATGTTGGCCCAGAAGGC
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                                                                                                                            Sequence 7, Application US/10797893
Fublication No. US20040142397A1
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
FRIOR FILING DATE: 2000-11-28
FRIOR FILING DATE: 2000-11-28
FRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                          TGAGGAAAAGGAGAACCATTGTCCCACAATG 1559
                                               TGAGGAAAAGGAGAACCATTGTCCCACAATG 1535
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 1461; Conservative
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; TYPE: DNA
; ORGANISM: Human
US-10-797-893-7
                                                                                                        RESULT 3
US-10-797-893-7
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APPLICANT: Craig Rosen,
PEPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101

Sequence 288, Application US/09925300 Patent No. US20020151681A1 GENERAL INFORMATION:

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94.3%; Score 1450.2;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1457; Conservative 7; Mismatches
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 288
LENGTH: 2104
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FEATURE:
NAME/KEY: misc feature
LOCATION: (44)
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LOCATION: (497)
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NAME/KEY: misc feature
LOCATION: (1373)
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                                                                                 Length 1115;
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                                                                                 DB 17;
                                                                                Score 1112.4;
Pred. No. 0;
0; Mismatches
                                                                                 72.3%;
99.9%;
                                                                              Query Match 72.3'
Best Local Similarity 99.9'
Matches 1113; Conservative
             ; LENGTH: 1115
; TYPE: DNA
; ORGANISM: Human
US-10-797-893-1
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                                                       TCGCCAGCGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCG
                                                                                            CACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGT
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Fublication No. US20040142397A1
GENERAL INPORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and met;
TITLE OF INVENTION: their use
FILE REFERRENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT APPLICATION NUMBER: US/09/24,224
FRIOR FILING DATE: 2004-03-09
FRIOR FILING DATE: 2000-11-28
FRIOR FILING DATE: 2000-11-28
FRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
                     484 GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATTCCGAGAAGACTGCCGGGGGAATATC
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US-09-96-23-131
US-09-96-23-131

Sequence 131 Application US/09960253

Fatent No. US20020123619A1

GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/960,253
CURRENT FILING DATE: 2001-09-20

NUMBER OF SEQ ID NOS: 187

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 131

LENGTH: 491
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                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/10797893
; Beduence 5, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; TITLE OF INVENTION: their use
; TILE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR PILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FREESEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                 1081 ACTITGCTGCCAGGTCCAAGGAGGTGATCAATCG 1114
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US-10-797-893-5
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                                                    1147 CCTTGGGACCTGTTAAGCTGTCTCAGAAGAATTGCTTGGTCCACCAGAGGAAGAAGAGAG
                                                                                                                                                           1207 CCCGAGGCCCTGAGGAAGAGGAGATTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTG
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  Gaps
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  Indels
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publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Britis, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER;
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-02
PRIOR FILING DATE: 2000-13-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FRAESEQ for Windows Version 4.0

LEASTH. 24525
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  Mismatches
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  Conservative
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CORGANISM: Homo sapiens
US-10-087-192-1180
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US-10-087-192-1180
Matches 380;
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                                                                                                                                                                                                                                                                                        240 GGCAGCTCCAGCCTCCCCAGAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGA 299
                                                                                                                                                                                                                                                                                                                                                                                                  300 CCCGGCCATGCTGGAGCGCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGGAGCCA 359
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Pred. No. 1.1e-104;
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APPLICANT: Innis, Michael A.
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reduction, Pablo Dominiquez
APPLICANT: Reduction, Christoph
APPLICANT: Randazco, Filippo
APPLICANT: Randazco, Filippo
APPLICANT: Ranedy, Giulia C.
APPLICANT: Raneon, George
APPLICANT: David
APPLICANT: Damanco, Radoje
APPLICANT: Dramanco, Radoje
APPLICANT: Dramanco, Radoje
APPLICANT: Dramanco, Radoje
APPLICANT: Dramanco, Snezana
APPLICANT: Leshkowitz, Dena
APPLICANT: Lebat, Ivan
APPLICANT: Lebat, Ivan
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garche, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garche, Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Williams, Lewis T.
APPLICANT: Bscobedo, Jaime
APPLICANT: Bscobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Garcia, Pablo Dominiguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Rennedy, Giulia C.
APPLICANT: Kennedy, Giulia C.
APPLICANT: Emnedy, Giulia C.
APPLICANT: Dranac, Radoje
APPLICANT: Dranac, Radoje
APPLICANT: Dranac, Radoje
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
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Publication No. US20030044783A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.5%;
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ORGANISM: Homo sapiens
US-09-803-719-1937
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Best Local Similarity
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LENGTH: 386
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2939 AGGTATTAGACCTCTTGGATCCTGCATCAGGAGACCTCGTGATCCGCGAAGACTGCCGAG 2998
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37 GCCTGGAATTCAATATCGCGGTCGATAGAGTGTAAACGGCCCGGAACCAGCCGGTAATCT
                                                                 260 CAAATACCAGTTTGATGCCTTCTATGGGGAGAGAGTACTCAGCAGGACATCTATGCAGG
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                                                                                                            97 cccrrraccreteccrreccrrracacaeccaraesaesaecrececereaearaecerec
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Publication No. US202010182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER.
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR PRILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PELING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SEQ ID NO 1177
LENGTH: 24291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 262.4; DB 13;
Pred. No. 4e-69;
0; Mismatches 61;
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OTHER INFORMATION: n = A,T,C or
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ilarity 73.8%;
Conservative
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LOCATION: (1)...(24291)
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Best Local Similarity
Matches 385; Conserv
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US-10-087-192-1177
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9493 CCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGAGGCCGCAGACAGGGGCGAGGACCT 2552
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                                                                          2553 GGGAAGCCCAGGAGCCTGAGCTAAGCACGAGACCTTTGTTCTTACCCCCCAGGTGGACCAG
                                                                                                                                                          GGGTCAGAGGACAACCGGCGCACAGGCAACAAGGGCCCTTCGGCTAAAAGAGAGTGGAGCC
                                                                                                                                                                                                                                                                ATCAACACCTCCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCT
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; Publication No. US20030073623A1
; GENERAL INPORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; FILE REPRENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR PELLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FREESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Indels
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Pred. No. 1.7e-70;
0; Mismatches 95;
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; LOCATION: (1)...(464)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31705
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Matches 333; Conservative
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US-09-918-995-31705
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LENGTH: 464
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Sequence 24303, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: HOWENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITLE OF INVENTION: HUMBESION ANALYSIS TWO

TITLE OF INVENTION: WIMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARER: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 24303
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             938 TCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAGCTCACTCGCCTATTGCAGGAC 995
                                                          214 TCAGGGCCTCCCTCGTGTACCTTATCGGACAGCAGCAGCTCACTCGCCTATTGCAGGTC 271
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OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 6.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: SWISSPROT HIT: Q14807, EVALUE 5.00e-37

OTHER INFORMATION: BST HUMAN HIT: BE382882.1, EVALUE 1.00e-125

US-10-029-386-24303
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Pred. No. 5.4e-60;
0; Mismatches 1; Indels 0;
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Sequence 249, Application US/10108260A

Sequence 249, Application US/10108260A

GENERAL INFORMATION:
TITLE OF INVENTION: NO. US20040005560Alel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 249
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Best Local Similarity 99.6%;
Matches 231; Conservative C
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ORGANISM: Homo sapiens
FEATURE:
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US-10-029-386-24303
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OTHER OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CURRENT APPLICATION: BXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10603
LENGTH: 531
3059 AGCACTTCCAGCCAGTAGAAATCGAGCTGTAGGAGCCACCCGGCTTAACCAGGGCT 3118
                                                                                                                                                                                                                                                                                                            3238
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                                                                                                                                                                                                                                                                                                     GAACGTTTGGCCCCATTTCGCCAGCGAGAAAACTCTACCTGATTGACTTGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3299 TCAGAGGACAACCGTCGCACAGGCAACCAGGGCATTCGGCTCAAAGAGAGCGGAGCCATC
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EXPRESSED IN FETAL LIVER, SIGNAL = 6.6

EXPRESSED IN BRAIN, SIGNAL = 1.3

EXPRESSED IN BONE MARROW, SIGNAL = 2.7

NT HIT: ABOIT 334.1, EVALUE 0.00e+00

SMISSPROT HIT: D14807, EVALUE 2.00e-36

EST_HUMAN HIT: BF975048.1, EVALUE 1.00e-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.2%; Score 233.2; DB 15; Length 98.7%; Pred. No. 9.9e-61; ive 0; Mismatches 3; Indels
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                                                                                                       730 CCTCCCGCAGTCATGCTGTGCTCCTGGTCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10603, Application US/10029386; Publication No. US20030194704A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 235; Conservative
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ORGANISM: Homo sapiens
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Burgess, Catherine E., Chant, John S., Chaudhuri, Amitabha, Dibippo, Vincent A., Edinger, Shlomit R.,

Gerlach, Valerie, Ji, Weizhen, Kekuda, Ramesh, Khramtsov, Nikolai,

Ellerman, Karen, Gangolli, Esha A., Gorman, Linda,

Eisen, Andrew,

Li, Li, Malyankar, Uriel M., MacDougall, John R.,

Miller, Charles E., Millet, Isabelle,

Mezes, Peter S.

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APPLICANT:
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                                                                                                Gaps
                                                                                       21;
            DB 16; Length 2095;
    Score 185.6; DB 16; Length
Pred. No. 6.1e-46;
0; Mismatches 379; Indels
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Query Match
Best Local Similarity 53.7%;
Matches 464; Conservative
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Padigaru, Muralidhara

Luca,

Rastelli,

Ooi, Chean Eng, Ort, Tatiana,

Rieger, Daniel K., Rothenberg, Mark E. Shenoy, Suresh G., Patturajan, Meera,

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Prior Application data removed - See File Wrapper or PALM.
SEQ ID NOS: 673
                                                                                                                                                        IITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 156.8; DB 16; Length 3374;
Pred. No. 4.8e-37;
0; Mismatches 317; Indels 18;
                                                                                                                                                                              FILE REFERENCE: 21402-480C
CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-12-30
PRIOR FILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-27
PRIOR PILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-11-30
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PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-13
PRIOR PILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-11-20
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/334,421
Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, Jr., Raymond
Vernet, Corine A.M.,
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                                                                                                    Zerhusen, Bryan D.
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Best Local Similarity 54.1%;
Matches 395; Conservative
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SEQ ID NO 301
LENGTH: 3374
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NUMBER OF
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; Sequence 301, Application US/10287226; Publication No. US20040086875A1; GENERAL INFORMATION:

US-10-287-226-301

APPLICANT: Agee, Michele L., APPLICANT: Alsobrook, John P., APPLICANT: Berghs, Constance,

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986 ATTGCAGGACTCTCTGGGTGGCTCACAGTATCCTTATTGCCAAACATTGCCCCTGA 1045
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Search completed: November 11, 2004, 01:20:38 Job time : 825.883 secs

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BX397059 602638562

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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSFORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CK615781 2057 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DK012YE23 of HeLa cells Cot 25-normalized of Homo sapiens (human).
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Submitted (20-UTL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2057)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/db_xref="taxon:9606"
/clone="CSODK012VE23"
/tisbue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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99.9%; Pred. No. 0;
ive 0; Mismatches
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BM561588
BU860011
AL576578
BU521359
BQ953445
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AL559752
BX404325
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BG686012
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CR615781.1 G1:50496588
HTC; CNSLT_CDNA.
HOMO sapiens (human)
HOMO sapiens
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AUTHORS
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AL578338
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BX337406 E
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                  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             32822875 seqs, 18219865908 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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99b_htc:

99b_est43:

99b_est64:

99b_est65:

95b_gs81:

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/tissue type="Placenta
/plasmid="pCMVSPORT_6"
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/db_xref="taxon:9606"
/clone="CS0DI009YJ01"
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CR590974 CR590974 Clone CS0DI009YJ01 of Placenta Cot 25-normalized of Homo sapiens (human).

CR590974.1 GI:50471781

HTC; CNSIT_CNNA.

HOMO sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

EL (bases 1 to 2025)

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Full-length cDNA libraries and normalization

L Unpublished
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 1919 JONE EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr.

- Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, doubble-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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GCCTTGGGACCTGTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGA
                                                       GCCCGAGGCCCTGAGGAAGAGGAGTTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCT
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Genoscope.

Direct Submission

Submitsed (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr | 18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoN with sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitogen.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Li, Wasea 1 to 2016)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
 1261 CAGCCCCTACAGAAGCTAAGCATGCATGAACCGGCCATGCTGGAGCGCCTCCTCAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.1%; Score 1462.8; DB 3; Length 2016;
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|mol_type="mRNA"
|db_xref="taxon:9606"
|clone="CSODI040Y106"
|/tissue_type="Placenta Cot/plasmid="pcMVSPORT_6"
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                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase 1 & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2055)
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Please visit our web site for further details
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|strain="C57BL/6J"
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Nature 409, 685-690 (2
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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7.22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegger.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Enxylopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshina, Yoshino, M., Muramatsu, M., and Hayashizaki, Y. Direct Submission
Submitted (16-APR-2002) Yoshinide Hayashizaki, The Institute of
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URL:http://genome.gsc.riken.jp/
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Location/Qualifiers
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of 60,770 full-length cDNAs

Linative 420, 563-573 (2002)

E (Dases I to 2056)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Furuno, M., Hanaqaki, T., Harai, A., Hayatsu, N., Hiramoto, K., Hiranoto, K., Hiranoto, K., Inthi, Y., Itoh, M., Izawa, M., Kasukawa, T., Mori, F., Imotani, K., Ishii, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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     TCTGTTGAGTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAAGGA
                                                 CCTAGAGATTGAGAGGCTTAAGACGAAAGCAAAAAGAACTGGAGGCCCAAGATGTTGGCCCA
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
wehr. Enzymol. 303, 19-44 (1999)
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sapiens (human)

Homo

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1124)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Pull.-Bength cubr. C., Jessee, J. and rormalization Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31267547. Contact: Genoscope - Centre National de Sequencage Genoscope - Gentre National de Sequencage

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DI009CE01QP1&c=7766.r. Location/Qualifiers

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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                             CCTCCTGGACCCCTGCTTCGGGRGACCTGGTAATCCGAGAAGACTGCCGGGGGRATATCCT
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GATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCCT
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                                                                                  CCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATCCT
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BX337406 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens clone CSODI041XII3 5-PRIME, mRNA sequence.

BX337406, GI:46274820
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODIO41ABO7QP1&c=7766.r.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Phll-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                181 CCCCTGTGTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACC
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I (Dases I to 1083)

I (W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31283903.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BRail: seqret@genoscope.cns.fr, Web: www.genoscope.cns.fr

Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EccRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen

This sequence belongs to sequence cluster 7766.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?e=CSODG005CF06QP1&c=7766.r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODGOOSYL11"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/clone="line="RAMOS CELL LINE"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                  AAGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGGAAGTGGTAGATGCGCTGA
                                                                   AAGAGAGTGGAGCCATCAACACCTCCTKTTTGTCCTGGGCAAAGTGGTAGATGCGCTGA
                                                                                                                  ATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAACCAGCTCGCCTATTGCAGGACT
                                                                                                                                                                      ATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAGCTCACTCGCCTATTGCAGGACT
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Genoscope - Centre National de Sequencage
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BM 191 91006 EVRY cedax - France
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library,
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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COT 25-NORMALIZED Homo sapiens
mRNA sequence.
                             AGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 AGCAAGCTCACTCGCCTATTGCAGGACTCTTGGGTGGSTCAGCCACATGTATCCTTAT
                                                                                           GGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGC
                                                                                                                      541 GGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGC
                                                                                                                                                                                GGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCT
                                                                                                                                                                                                                      601 GCCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCT
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                                                                                                                                                                                                                                                                                                                                                         TTCGCCAGCGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                  721 TTCGCCAGCGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                850 GCACAGGCAACAAGAGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODK012AC12QP1&c=7766.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On May 5, 2003 this sequence version replaced gi:30368690.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; E
Catarrhini; Hominidae;
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Mammalia, Butheria, Primates, Catarrhini, Hon
1 (bases 1 to 959)
Li,W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                  On May 2, 2003 this sequence version replaced gi:30337600.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549
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                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="PLACENTA COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 4.8e-248;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity 98.6%;
Matches 1003; Conservative
                                             sapiens (human)
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                GATCTCAGGAGCTGGTCGCTGTCGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCC
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                                                                                                        0; Indels
                                                                                    Length
                                                                                   Score 942; DB 5; I
Pred. No. 2.4e-238;
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99.9%;
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Matches 953;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMYSORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                         BX354166 BX354166 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODC015YH04 5-PRIME, mRNA sequence.
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/note="ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                             959
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                                                                                                                                                                                                                                                                                                                                                       Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gi:30373827
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Pred. No. 3.2e-236;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  M Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Bukaryota; Metazoa; Chordata; Catarrhini; Hominid
1 (Dases 1 to 958)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:
                                                                                                                                                                                                                                 BX354166.2 GI:46304510
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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957 CCTTATCGGGACAGCAGGTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCAC 1016
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/db xref="taxon:9606"
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/cloned inb="brain; Vector: pOTB7; Site_1: XhoI; Site_2: Cloned into EcoRI, XhoI sites using the following 5' adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zah-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GGCAGCCCAGAGCAACCTGGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACA
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I (bases I to 1031)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clond through the I.M.A.G.E. Consortium/LLNL http://image.lln.gov
Plate: LLCM1948 row: 1 column: 06
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Homo Homo

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

source

FEATURES

176 600 836 ,099 896 720 926 780

400 425 460 485 520 545 580 605 640 665

280 305 340

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BX376199 1004 bp mRNA linear EST 27-APR-2004
BX376199 Homo sapiens NEUROBLASTOWA COT 25-NORWALIZED Homo sapiens
CDNA clone CSODC024YA10 5-PRIME, mRNA sequence.
BX376199
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                       GATCCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAAGAAC
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30452476. Contact: Genoscope - Centre National de Sequencage Genoscope - Genere National de Sequencage
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1 (bases 1 to 999)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

3 Full-length cDNA libraries and normalization

3 In pubblished (2001)

3 On Peb 15, 2001 this sequence version replaced gi:31283900.

3 Contact: Genoscope — Centre National de Sequencage

3 Genoscope — Centre National de Sequencage

3 Bp 191 91006 EVRY cedax - France

3 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

3 Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BCORV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
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/mol_type="mRNA"
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/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcORY sites of the pcMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                           AL559769 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA CLONE CSODGOOSYF11 5-PRIME, mRNA sequence.
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AL559769.3 GI:46185141
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CCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCAC
                                                                         GCGCGGGCGGCTCGACGCAGCAGAGGCGACGCGAGATGGCGGCAGCTTCAGCGGCGCG
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODG005CC06QPl&c=7766.
Location/Qualifiers
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96.8%; Pred. No. 7e-233;
ive 22; Mismatches 8
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Homo sapiens
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AL559769
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/clone="Introduction" / /clone="Introduction" / /clone="Introduction" / /clone="Introduction" / /clone="Introduction" / /clone | /clone=|Introduction" / /clone=|Introduction" / /clone=|Introduction" / /clone=|Organ: ovary(pool of 3); Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to 49 yo. Library is oloned (EcoRV site is destroyed upon cloning). Average insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA linear EST 20-FEB-2002 sapiens cDNA clone IMAGE:5723623
                                                                                                                                                                                                                                                                                                   CCGCCGCACAGGCAACAAGGSCTTCGGCTAAAAAGAGAGTGGAGCCATCAACACCCTCCC 911
                                                                                                                                                                                              CCCATTTCGCCAGCGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAA 851
        672 TGAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCA 731
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 1019)

Si NiH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llhl.gov

Plate: LLAM12711 row: j column: 08

High quality sequence stop: 688.
                                                                                                            732 GCGCTCCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGC
                                                                                                                                                                                                                                                                                                                                                                               912 TGTTTGTCCTKGGCAAAGTGGTAGATGCGCTGAATCAGGG-CTCCCTCGTGTA-CTTATC
                                                                                                                                                                   CCCATTTCGCCAGCGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAA
                                                                                                                                                                                                                                                                       845 CCGGCGCACAGGCAACAAGGGCCTTCGGCT-AAAAGAGAGTGGAGCCATCAACACCTCCC
                                                           GCGCTCCTCCCCCCATCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGC
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Best Local Similarity 97.5%; Pred. No. 1.4e-229;
Matches 965; Conservative 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENCOURT_6491037 NIH_MGC_125 Homo 5', mRNA sequence.
BMS46877.1 GI:18780186
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/db_xref="taxon:9606"
/clone="CSOGYANO"
/tissue type="NBUROBLASTOWA COT 25-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED"
/clone lib="Homo sapiens of the organism of the organism of the pomysport of the organism of the pomysport of the organism of the pomysport of the vector. Library was normalized."
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                                                                                                                                                                                      For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODC024BA05QP1&c=7766.r. Location/Qualifiers
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